GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 21, 2004, 09:44:42 ; Search time 35 Seconds
(without alignments)
331.782 Million cell updates/sec

Title: US-10-010-709-1
Perfect score: 259
Sequence: 1 KSCCRSTLGRNCYNLCRVRG.....AGVCRCKLTSSGKCPTGFPK 45

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	224	86.5	137	10	Q9T0P1	Q9t0p1 triticum ae
2	214	82.6	136	10	Q9T0P2	Q9t0p2 triticum ae
3	214	82.6	136	10	Q43205	Q43205 triticum ae
4	208	80.3	136	10	Q9ZNY5	Q9zny5 secale cere
5	166.5	64.3	137	10	Q9S9D7	Q9s9d7 hordeum vul
6	163.5	63.1	107	10	Q43226	Q43226 tulipa gesn
7	163.5	63.1	114	10	Q43225	Q43225 tulipa gesn
8	160.5	62.0	114	10	Q9S9A0	Q9s9a0 viscum albu
9	157.5	60.8	137	10	Q8LT02	Q8lt02 avena sativ
10	154.5	59.7	137	10	Q8LT03	Q8lt03 avena sativ
11	145.5	56.2	137	10	Q42838	Q42838 hordeum vul
12	143.5	55.4	112	10	Q43227	Q43227 tulipa gesn
13	143.5	55.4	142	10	Q8LT00	Q8lt00 avena sativ
14	141.5	54.6	121	10	Q43224	Q43224 tulipa gesn
15	140.5	54.2	137	10	Q8H0Q5	Q8h0q5 hordeum vul
16	136.5	52.7	137	10	Q8LT01	Q8lt01 avena sativ
17	135	52.1	136	10	Q8LSZ9	Q8lsz9 avena sativ
18	126.5	48.8	111	10	Q9S9A2	Q9s9a2 viscum albu
19	124	47.9	124	10	Q41609	Q41609 tulipa gesn
20	118.5	45.8	130	10	Q9S975	Q9s975 crambe abys
21	118	45.6	115	10	Q9S9A1	Q9s9a1 viscum albu
22	110	42.5	90	10	Q9S6Y2	Q9s6y2 triticum ae
23	109.5	42.3	133	10	Q9SBK8	Q9sbk8 brassica ra
24	109.5	42.3	135	10	Q9S974	Q9s974 crambe abys
25	98.5	38.0	135	10	Q9S977	Q9s977 crambe abys
26	96.5	37.3	134	10	Q9S976	Q9s976 crambe abys
27	92	35.5	135	10	Q8LT04	Q8lt04 oryza sativ
28	88.5	34.2	133	10	Q9S980	Q9s980 crambe abys
29	86	33.2	118	10	Q9C7S9	Q9c7s9 arabidopsis
30	86	33.2	122	10	Q8LCH6	Q8lch6 arabidopsis
31	86	33.2	134	10	Q42596	Q42596 arabidopsis
32	83.5	32.2	134	10	Q9S981	Q9s981 crambe abys
33	79.5	30.7	135	10	Q8VZK8	Q8vzk8 arabidopsis
34	78.5	30.3	135	10	Q9ZUL0	Q9zul0 arabidopsis
35	76	29.3	1574	11	O88281	O88281 rattus norv
36	75.5	29.2	118	10	Q9S979	Q9s979 crambe abys
37	69.5	26.8	1664	5	Q9TVQ2	Q9tvq2 caenorhabdi
38	67	25.9	425	6	O02661	O02661 bos taurus
39	67	25.9	5146	6	Q8SPM4	Q8spm4 bos taurus
40	66.5	25.7	594	5	Q9W0A1	Q9w0a1 drosophila
41	66.5	25.7	1246	4	O75095	O75095 homo sapien
42	66	25.5	2731	5	Q9VJT5	Q9vjt5 drosophila
43	66	25.5	3367	5	Q9XZC9	Q9xzc9 drosophila
44	66	25.5	3375	5	Q8IP51	Q8ip51 drosophila
45	65.5	25.3	134	10	Q9FIW2	Q9fiw2 arabidopsis

ALIGNMENTS

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RESULT 1
Q9T0P1
ID   Q9T0P1      PRELIMINARY;      PRT;   137 AA.
AC   Q9T0P1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Alpha purothionin precursor.
GN   PUR-B1.
OS   Triticum aestivum (Wheat).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Triticeae; Triticum.
OX   NCBI_TaxID=4565;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Chinese spring;
RA   Van Campenhout S., Sagi L., Vander Stappen J., Volckaert G.;
RT   "Characterisation of type-I thionin loci from the A, B, D and R
RT   genomes of wheat and rye.";
RL   Theor. Appl. Genet. 96:80-86(1998).
CC   -!- FUNCTION: THIONINS ARE SMALL PLANT PROTEINS WHICH ARE TOXIC TO
CC       ANIMAL CELLS. THEY SEEM TO EXERT THEIR TOXIC EFFECT AT THE LEVEL
CC       OF THE CELL MEMBRANE. THE PRECISE FUNCTION, IN PLANTS, OF THESE
CC       PROTEINS IS NOT KNOWN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PLANT THIONIN FAMILY.
DR   EMBL; X96446; CAA65313.1; -.
DR   HSSP; P01544; 2PLH.
DR   InterPro; IPR001010; Thionin.
DR   Pfam; PF00321; plant_thionins; 1.
DR   PROSITE; PS00271; THIONIN; 1.
KW   Plant defense; Plant toxin; Signal; Thionin; Toxin.
FT   SIGNAL        1     27       POTENTIAL.
FT   CHAIN        28     72       POTENTIAL.
SQ   SEQUENCE   137 AA;  14630 MW;  14039F238005400B CRC64;

  Query Match          86.5%;  Score 224;  DB 10;  Length 137;
  Best Local Similarity  84.4%;  Pred. No. 4.2e-23;
  Matches   38;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;
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Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              ||||||||||||||||| ||||||||||||::|   || ||||
Db         28 KSCCRSTLGRNCYNLCRARGAQKLCAGVCRCKISSGLSCPKGFPK 72


RESULT 2
Q9T0P2
ID   Q9T0P2      PRELIMINARY;      PRT;   136 AA.
AC   Q9T0P2;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Beta purothionin precursor.
GN   PUR-A1.
OS   Triticum aestivum (Wheat).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Triticeae; Triticum.
OX   NCBI_TaxID=4565;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Chinese spring;
RA   Van Campenhout S., Sagi L., Vander Stappen J., Volckaert G.;
RT   "Characterisation of type-I thionin loci from the A, B, D and R
RT   genomes of wheat and rye.";
RL   Theor. Appl. Genet. 96:80-86(1998).
CC   -!- FUNCTION: THIONINS ARE SMALL PLANT PROTEINS WHICH ARE TOXIC TO
CC       ANIMAL CELLS. THEY SEEM TO EXERT THEIR TOXIC EFFECT AT THE LEVEL
CC       OF THE CELL MEMBRANE. THE PRECISE FUNCTION, IN PLANTS, OF THESE
CC       PROTEINS IS NOT KNOWN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PLANT THIONIN FAMILY.
DR   EMBL; X96445; CAA65312.1; -.
DR   HSSP; P01543; 1BHP.
DR   InterPro; IPR001010; Thionin.
DR   Pfam; PF00321; plant_thionins; 1.
DR   PROSITE; PS00271; THIONIN; 1.
KW   Plant defense; Plant toxin; Signal; Thionin; Toxin.
FT   SIGNAL        1     27       POTENTIAL.
FT   CHAIN        28     72       POTENTIAL.
SQ   SEQUENCE   136 AA;  14715 MW;  90B5C8155730126E CRC64;

  Query Match             82.6%;  Score 214;  DB 10;  Length 136;
  Best Local Similarity   82.2%;  Pred. No. 9.9e-22;
  Matches   37;  Conservative    1;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              ||||:|||||||||||| |||||||| ||||||||   ||  |||
Db         28 KSCCKSTLGRNCYNLCRARGAQKLCANVCRCKLTSGLSCPKDFPK 72


RESULT 3
Q43205
ID   Q43205      PRELIMINARY;      PRT;   136 AA.
AC   Q43205;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Alpha-1 purothionin.
OS   Triticum aestivum (Wheat).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Triticeae; Triticum.
OX   NCBI_TaxID=4565;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Chinese Spring;
RA   Inagaki A., Matsuoka Y., Tsunewaki K.;
RT   "Unpublished.";
RL   Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: THIONINS ARE SMALL PLANT PROTEINS WHICH ARE TOXIC TO
CC       ANIMAL CELLS. THEY SEEM TO EXERT THEIR TOXIC EFFECT AT THE LEVEL
CC       OF THE CELL MEMBRANE. THE PRECISE FUNCTION, IN PLANTS, OF THESE
CC       PROTEINS IS NOT KNOWN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PLANT THIONIN FAMILY.
DR   EMBL; D84390; BAA12336.1; -.
DR   HSSP; P01543; 1BHP.
DR   InterPro; IPR001010; Thionin.
DR   Pfam; PF00321; plant_thionins; 1.
DR   PROSITE; PS00271; THIONIN; 1.
KW   Plant defense; Plant toxin; Thionin; Toxin.
SQ   SEQUENCE   136 AA;  14542 MW;  B4018F414E226B9F CRC64;

  Query Match             82.6%;  Score 214;  DB 10;  Length 136;
  Best Local Similarity   82.2%;  Pred. No. 9.9e-22;
  Matches   37;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              |||||:|||||||||||| ||||||| |||||||   || ||||
Db         28 KSCCRTTLGRNCYNLCRSRGAQKLCSTVCRCKLTSGLSCPKGFPK 72


RESULT 4
Q9ZNY5
ID   Q9ZNY5      PRELIMINARY;      PRT;   136 AA.
AC   Q9ZNY5;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Purothionin precursor.
GN   PUR-RL.
OS   Secale cereale (Rye).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Triticeae; Secale.
OX   NCBI_TaxID=4550;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Petkus;
RA   Van Campenhout S., Sagi L., Vander Stappen J., Volckaert G.;
RT   "Characterisation of type-I thionin loci from the A, B, D and R
RT   genomes of wheat and rye.";
RL   Theor. Appl. Genet. 96:80-86(1998).
CC   -!- FUNCTION: THIONINS ARE SMALL PLANT PROTEINS WHICH ARE TOXIC TO
CC       ANIMAL CELLS. THEY SEEM TO EXERT THEIR TOXIC EFFECT AT THE LEVEL
CC       OF THE CELL MEMBRANE. THE PRECISE FUNCTION, IN PLANTS, OF THESE
CC       PROTEINS IS NOT KNOWN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PLANT THIONIN FAMILY.
DR   EMBL; X96449; CAA65316.1; -.
DR   HSSP; P01543; 1BHP.
DR   InterPro; IPR001010; Thionin.
DR   Pfam; PF00321; plant_thionins; 1.
DR   PROSITE; PS00271; THIONIN; 1.
KW   Plant defense; Plant toxin; Signal; Thionin; Toxin.
FT   SIGNAL        1     27       POTENTIAL.
FT   CHAIN        28     72       POTENTIAL.
SQ   SEQUENCE   136 AA;  14633 MW;  799F5DCBE07EA735 CRC64;

  Query Match             80.3%;  Score 208;  DB 10;  Length 136;
  Best Local Similarity   80.0%;  Pred. No. 6.6e-21;
  Matches   36;  Conservative    1;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              ||||:|||||||||||| ||||||||  ||||| ||  ||  |||
Db         28 KSCCKSTLGRNCYNLCRTRGAQKLCANFCRCKLISSTSCPKEFPK 72


RESULT 5
Q9S9D7
ID   Q9S9D7      PRELIMINARY;      PRT;   137 AA.
AC   Q9S9D7;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Thionin.
OS   Hordeum vulgare (Barley).
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OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Triticeae; Hordeum.
OX   NCBI_TaxID=4513;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92167966; PubMed=1371580;
RA   Bunge S., Wolters J., Apel K.;
RT   "A comparison of leaf thionin sequences of barley cultivars and wild
RT   barley species.";
RL   Mol. Gen. Genet. 231:460-468(1992).
CC   -!- FUNCTION: THIONINS ARE SMALL PLANT PROTEINS WHICH ARE TOXIC TO
CC       ANIMAL CELLS. THEY SEEM TO EXERT THEIR TOXIC EFFECT AT THE LEVEL
CC       OF THE CELL MEMBRANE. THE PRECISE FUNCTION, IN PLANTS, OF THESE
CC       PROTEINS IS NOT KNOWN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PLANT THIONIN FAMILY.
DR   HSSP; P01543; 1BHP.
DR   InterPro; IPR001010; Thionin.
DR   Pfam; PF00321; plant_thionins; 1.
DR   PROSITE; PS00271; THIONIN; 1.
KW   Plant defense; Plant toxin; Thionin; Toxin.
SQ   SEQUENCE   137 AA;  14730 MW;  A582052B555B3646 CRC64;

  Query Match             64.3%;  Score 166.5;  DB 10;  Length 137;
  Best Local Similarity   58.7%;  Pred. No. 3.3e-15;
  Matches   27;  Conservative    6;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQK-LCAGVCRCKLTSSGKCPTGFPK 45
              |||| || ||||| ||  |  : :||| ||||: |  |||: :||
Db         29 KSCCKDTLARNCYNTCRFAGGSRPVCAGACRCKIISGPKCPSDYPK 74


RESULT 6
Q43226
ID   Q43226      PRELIMINARY;      PRT;   107 AA.
AC   Q43226;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Thionin class 1 precursor.
GN   THI1-3.
OS   Tulipa gesneriana.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae; Tulipa.
OX   NCBI_TaxID=13306;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Apeldoorn;
RA   Luyten R.M.J.M., Balk P.A., de Boer A.D.;
RL   Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: THIONINS ARE SMALL PLANT PROTEINS WHICH ARE TOXIC TO
CC       ANIMAL CELLS. THEY SEEM TO EXERT THEIR TOXIC EFFECT AT THE LEVEL
CC       OF THE CELL MEMBRANE. THE PRECISE FUNCTION, IN PLANTS, OF THESE
CC       PROTEINS IS NOT KNOWN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PLANT THIONIN FAMILY.
DR   EMBL; X81708; CAA57352.1; -.
DR   HSSP; P01544; 2PLH.
DR   InterPro; IPR001010; Thionin.
DR   Pfam; PF00321; plant_thionins; 1.
DR   PROSITE; PS00271; THIONIN; 1.
KW   Plant defense; Plant toxin; Signal; Thionin; Toxin.
FT   SIGNAL        1     18       POTENTIAL.
SQ   SEQUENCE   107 AA;  11356 MW;  91E4CF2B6DD2D7A2 CRC64;

  Query Match             63.1%;  Score 163.5;  DB 10;  Length 107;
  Best Local Similarity   58.7%;  Pred. No. 6.9e-15;
  Matches   27;  Conservative    7;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQK-LCAGVCRCKLTSSGKCPTGFPK 45
              |||||:|  |||||:||: |  : :||  | ||: |||||| |: |
Db         19 KSCCRNTTARNCYNVCRLPGTPRPVCAATCDCKIISSGKCPPGYEK 64


RESULT 7
Q43225
ID   Q43225      PRELIMINARY;      PRT;   114 AA.
AC   Q43225;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Thionin class 1 precursor.
GN   THI1-2.
OS   Tulipa gesneriana.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae; Tulipa.
OX   NCBI_TaxID=13306;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Apeldoorn;
RA   Luyten R.M.J.M., Balk P.A., de Boer A.D.;
RL   Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: THIONINS ARE SMALL PLANT PROTEINS WHICH ARE TOXIC TO
CC       ANIMAL CELLS. THEY SEEM TO EXERT THEIR TOXIC EFFECT AT THE LEVEL
CC       OF THE CELL MEMBRANE. THE PRECISE FUNCTION, IN PLANTS, OF THESE
CC       PROTEINS IS NOT KNOWN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PLANT THIONIN FAMILY.
DR   EMBL; X81707; CAA57351.1; -.
DR   HSSP; P01544; 2PLH.
DR   InterPro; IPR001010; Thionin.
DR   Pfam; PF00321; plant_thionins; 1.
DR   PROSITE; PS00271; THIONIN; 1.
KW   Plant defense; Plant toxin; Signal; Thionin; Toxin.
FT   SIGNAL        1     18       POTENTIAL.
SQ   SEQUENCE   114 AA;  11975 MW;  3105DAC0130CE8D4 CRC64;

  Query Match             63.1%;  Score 163.5;  DB 10;  Length 114;
  Best Local Similarity   58.7%;  Pred. No. 7.3e-15;
  Matches   27;  Conservative    7;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQK-LCAGVCRCKLTSSGKCPTGFPK 45
              |||||:|  |||||:||: |  : :||  | ||: |||||| |: |
Db         19 KSCCRNTTARNCYNVCRLPGTPRPVCAATCDCKIISSGKCPPGYEK 64


RESULT 8
Q9S9A0
ID   Q9S9A0      PRELIMINARY;      PRT;   114 AA.
AC   Q9S9A0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Thionin.
OS   Viscum album (European mistletoe).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Santalales; Viscaceae; Viscum.
OX   NCBI_TaxID=3972;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94122387; PubMed=8292787;
RA   Schrader-Fischer G., Apel K.;
RL   Plant Mol. Biol. 23:1233-1242(1993).
CC   -!- FUNCTION: THIONINS ARE SMALL PLANT PROTEINS WHICH ARE TOXIC TO
CC       ANIMAL CELLS. THEY SEEM TO EXERT THEIR TOXIC EFFECT AT THE LEVEL
CC       OF THE CELL MEMBRANE. THE PRECISE FUNCTION, IN PLANTS, OF THESE
CC       PROTEINS IS NOT KNOWN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PLANT THIONIN FAMILY.
DR   HSSP; P01544; 2PLH.
DR   InterPro; IPR001010; Thionin.
DR   Pfam; PF00321; plant_thionins; 1.
DR   PROSITE; PS00271; THIONIN; 1.
KW   Plant defense; Plant toxin; Thionin; Toxin.
SQ   SEQUENCE   114 AA;  11981 MW;  D30BFC724907CE7D CRC64;

  Query Match             62.0%;  Score 160.5;  DB 10;  Length 114;
  Best Local Similarity   56.5%;  Pred. No. 1.9e-14;
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  Matches   26;  Conservative    7;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQK-LCAGVCRCKLTSSGKCPTGFPK 45
              |||||:| |||||| ||| |  : :|| :| ||: |  |||  :|:
Db         27 KSCCRNTTGRNCYNACRVPGTPRPVCASLCDCKIISGSKCPADYPR 72


RESULT 9
Q8LT02
ID   Q8LT02      PRELIMINARY;      PRT;   137 AA.
AC   Q8LT02;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Leaf thionin Asthi2.
GN   ASTHI2.
OS   Avena sativa (Oat).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Aveneae; Avena.
OX   NCBI_TaxID=4498;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Zensin;
RX   MEDLINE=22054133; PubMed=12059099;
RA   Iwai T., Kaku H., Honkura R., Nakamura S., Ochiai H., Sasaki T.,
RA   Ohashi Y.;
RT   "Enhanced Resistance to Seed-Transmitted Bacterial Diseases in
RT   Transgenic Rice Plants Overproducing an Oat Cell-Wall-Bound Thionin.";
RL   Mol. Plant Microbe Interact. 15:515-521(2002).
DR   EMBL; AB072339; BAB93113.1; -.
DR   InterPro; IPR001010; Thionin.
DR   Pfam; PF00321; plant_thionins; 1.
DR   PROSITE; PS00271; THIONIN; 1.
SQ   SEQUENCE   137 AA;  14795 MW;  53CB63A48A5DDBBC CRC64;

  Query Match             60.8%;  Score 157.5;  DB 10;  Length 137;
  Best Local Similarity   54.3%;  Pred. No. 5.7e-14;
  Matches   25;  Conservative    7;  Mismatches   13;  Indels    1;  Gaps    1;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQK-LCAGVCRCKLTSSGKCPTGFPK 45
              ||||: |  |||||:||: |  : :||  ||||: |  |||  :||
Db         29 KSCCKDTTARNCYNVCRIPGTPRPVCATTCRCKIISGNKCPKDYPK 74


RESULT 10
Q8LT03
ID   Q8LT03      PRELIMINARY;      PRT;   137 AA.
AC   Q8LT03;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Leaf thionin Asthi1.
GN   ASTHI1.
OS   Avena sativa (Oat).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Aveneae; Avena.
OX   NCBI_TaxID=4498;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Zensin;
RX   MEDLINE=22054133; PubMed=12059099;
RA   Iwai T., Kaku H., Honkura R., Nakamura S., Ochiai H., Sasaki T.,
RA   Ohashi Y.;
RT   "Enhanced Resistance to Seed-Transmitted Bacterial Diseases in
RT   Transgenic Rice Plants Overproducing an Oat Cell-Wall-Bound Thionin.";
RL   Mol. Plant Microbe Interact. 15:515-521(2002).
DR   EMBL; AB072338; BAB93112.1; -.
DR   InterPro; IPR001010; Thionin.
DR   Pfam; PF00321; plant_thionins; 1.
DR   PROSITE; PS00271; THIONIN; 1.
SQ   SEQUENCE   137 AA;  14684 MW;  E91AE724C7621F68 CRC64;

  Query Match             59.7%;  Score 154.5;  DB 10;  Length 137;
  Best Local Similarity   52.2%;  Pred. No. 1.5e-13;
  Matches   24;  Conservative    8;  Mismatches   13;  Indels    1;  Gaps    1;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQK-LCAGVCRCKLTSSGKCPTGFPK 45
              ||||:  : |||||:||: |  : :||  ||||: |  |||  :||
Db         29 KSCCKDIMARNCYNVCRIPGTPRPVCATTCRCKIISGNKCPKDYPK 74


RESULT 11
Q42838
ID   Q42838      PRELIMINARY;      PRT;   137 AA.
AC   Q42838;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Thionin.
GN   BTH7.
OS   Hordeum vulgare (Barley).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Triticeae; Hordeum.
OX   NCBI_TaxID=4513;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Holtorf S., Schuetz C., Apel K., Bohlmann H.;
RT   "Specific and distinct expression patterns of two members of the
RT   thionin multigene family of barley in transgenic tobacco.";
RL   Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: THIONINS ARE SMALL PLANT PROTEINS WHICH ARE TOXIC TO
CC       ANIMAL CELLS. THEY SEEM TO EXERT THEIR TOXIC EFFECT AT THE LEVEL
CC       OF THE CELL MEMBRANE. THE PRECISE FUNCTION, IN PLANTS, OF THESE
CC       PROTEINS IS NOT KNOWN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PLANT THIONIN FAMILY.
DR   EMBL; L36883; AAA91048.1; -.
DR   HSSP; P01543; 1BHP.
DR   InterPro; IPR001010; Thionin.
DR   Pfam; PF00321; plant_thionins; 1.
DR   PROSITE; PS00271; THIONIN; 1.
KW   Plant defense; Plant toxin; Thionin; Toxin.
SQ   SEQUENCE   137 AA;  14676 MW;  7BDBAF7082F205BE CRC64;

  Query Match             56.2%;  Score 145.5;  DB 10;  Length 137;
  Best Local Similarity   52.2%;  Pred. No. 2.5e-12;
  Matches   24;  Conservative    6;  Mismatches   15;  Indels    1;  Gaps    1;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQK-LCAGVCRCKLTSSGKCPTGFPK 45
              ||||::| |||||| ||  |  : :||  | ||: |   ||  :||
Db         29 KSCCKNTTGRNCYNACRFAGGSRPVCATACGCKIISGPTCPRDYPK 74


RESULT 12
Q43227
ID   Q43227      PRELIMINARY;      PRT;   112 AA.
AC   Q43227;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Thionin class 1 precursor (Fragment).
GN   THI1-4.
OS   Tulipa gesneriana.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae; Tulipa.
OX   NCBI_TaxID=13306;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Apeldoorn;
RA   Luyten R.M.J.M., Balk P.A., de Boer A.D.;
RL   Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: THIONINS ARE SMALL PLANT PROTEINS WHICH ARE TOXIC TO
CC       ANIMAL CELLS. THEY SEEM TO EXERT THEIR TOXIC EFFECT AT THE LEVEL
CC       OF THE CELL MEMBRANE. THE PRECISE FUNCTION, IN PLANTS, OF THESE
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CC       PROTEINS IS NOT KNOWN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PLANT THIONIN FAMILY.
DR   EMBL; X81709; CAA57353.1; -.
DR   HSSP; P01542; 1CBN.
DR   InterPro; IPR001010; Thionin.
DR   Pfam; PF00321; plant_thionins; 1.
DR   PROSITE; PS00271; THIONIN; 1.
KW   Plant defense; Plant toxin; Signal; Thionin; Toxin.
FT   NON_TER       1      1
FT   SIGNAL        <1     12       POTENTIAL.
SQ   SEQUENCE   112 AA;  11863 MW;  BCF89C4A00FD0332 CRC64;

  Query Match             55.4%;  Score 143.5;  DB 10;  Length 112;
  Best Local Similarity   52.2%;  Pred. No. 4e-12;
  Matches   24;  Conservative    6;  Mismatches   15;  Indels    1;  Gaps    1;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQK-LCAGVCRCKLTSSGKCPTGFPK 45
              |||| ||  |||||:||  |  : :||  | ||: :  |||  :||
Db         13 KSCCPSTAARNCYNVCRFPGTPRPVCAATCGCKIITGTKCPPDYPK 58


RESULT 13
Q8LT00
ID   Q8LT00      PRELIMINARY;      PRT;   142 AA.
AC   Q8LT00;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Thionin Asthi4.
GN   ASTHI4.
OS   Avena sativa (Oat).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Aveneae; Avena.
OX   NCBI_TaxID=4498;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Zensin;
RX   MEDLINE=22054133; PubMed=12059099;
RA   Iwai T., Kaku H., Honkura R., Nakamura S., Ochiai H., Sasaki T.,
RA   Ohashi Y.;
RT   "Enhanced Resistance to Seed-Transmitted Bacterial Diseases in
RT   Transgenic Rice Plants Overproducing an Oat Cell-Wall-Bound Thionin.";
RL   Mol. Plant Microbe Interact. 15:515-521(2002).
DR   EMBL; AB072341; BAB93115.1; -.
DR   InterPro; IPR001010; Thionin.
DR   Pfam; PF00321; plant_thionins; 1.
SQ   SEQUENCE   142 AA;  15009 MW;  13CF1E57F5B94AAB CRC64;

  Query Match             55.4%;  Score 143.5;  DB 10;  Length 142;
  Best Local Similarity   54.3%;  Pred. No. 4.9e-12;
  Matches   25;  Conservative    7;  Mismatches   13;  Indels    1;  Gaps    1;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQK-LCAGVCRCKLTSSGKCPTGFPK 45
              ||||:||   ||||:||: || : :||| | |||      ||: :||
Db         29 KSCCKSTTAINCYNVCRLAGAPRPVCAGPCGCKLLDVTTCPSDWPK 74


RESULT 14
Q43224
ID   Q43224      PRELIMINARY;      PRT;   121 AA.
AC   Q43224;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Thionin class 1 precursor.
GN   THI1-1.
OS   Tulipa gesneriana.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae; Tulipa.
OX   NCBI_TaxID=13306;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Apeldoorn;
RA   Luyten R.M.J.M., Balk P.A., de Boer A.D.;
RL   Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: THIONINS ARE SMALL PLANT PROTEINS WHICH ARE TOXIC TO
CC       ANIMAL CELLS. THEY SEEM TO EXERT THEIR TOXIC EFFECT AT THE LEVEL
CC       OF THE CELL MEMBRANE. THE PRECISE FUNCTION, IN PLANTS, OF THESE
CC       PROTEINS IS NOT KNOWN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PLANT THIONIN FAMILY.
DR   EMBL; X81706; CAA57350.1; -.
DR   HSSP; P01544; 2PLH.
DR   InterPro; IPR001010; Thionin.
DR   Pfam; PF00321; plant_thionins; 1.
DR   PROSITE; PS00271; THIONIN; 1.
KW   Plant defense; Plant toxin; Signal; Thionin; Toxin.
FT   SIGNAL        1      18       POTENTIAL.
SQ   SEQUENCE   121 AA;  12761 MW;  37D5C7D557B6E0A9 CRC64;

  Query Match             54.6%;  Score 141.5;  DB 10;  Length 121;
  Best Local Similarity   54.3%;  Pred. No. 8e-12;
  Matches   25;  Conservative    5;  Mismatches   15;  Indels    1;  Gaps    1;

Qy          1 KSCCRSTLGRNCYNLCRVRGA-QKLCAGVCRCKLTSSGKCPTGFPK 45
              |||||:|  |||||:||: |  | |||  | |   ::| ||   ||
Db         19 KSCCRTTAARNCYNVCRLGGTPQTLCARTCDCIHITTGNCPRSHPK 64


RESULT 15
Q8H0Q5
ID   Q8H0Q5      PRELIMINARY;      PRT;   137 AA.
AC   Q8H0Q5;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Putative thionin.
OS   Hordeum vulgare (Barley).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Triticeae; Hordeum.
OX   NCBI_TaxID=4513;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Manchuria; TISSUE=Leaf;
RA   Kah B., Kogel K.H., Langen G.;
RT   "ORF of a leaf expressed barley thionin.";
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ508712; CAD48489.1; -.
SQ   SEQUENCE   137 AA;  14615 MW;  752F0489A4FEDC4E CRC64;

  Query Match             54.2%;  Score 140.5;  DB 10;  Length 137;
  Best Local Similarity   50.0%;  Pred. No. 1.2e-11;
  Matches   23;  Conservative    6;  Mismatches   16;  Indels    1;  Gaps    1;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQK-LCAGVCRCKLTSSGKCPTGFPK 45
              ||||::| ||||||  |    |  : :||  | ||: |    ||  :||
Db         29 KSCCKNTTGRNCYNACHFAGGSRPVCATACGCKIISGPTCPRDYPK 74


Search completed: January 21, 2004, 09:48:03
Job time : 37 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 21, 2004, 09:43:11 ; Search time 10 Seconds
(without alignments)
211.620 Million cell updates/sec

Title: US-10-010-709-1
Perfect score: 259
Sequence: 1 KSCCRSTLGRNCYNLCRVRG.....AGVCRCKLTSSGKCPTGFPK 45

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	259	100.0	127	1	THNA_HORVU	P01545 hordeum vul
2	225	86.9	136	1	THNB_HORVU	P21742 hordeum vul
3	224	86.5	126	1	THN1_WHEAT	P01544 triticum ae
4	214	82.6	136	1	THN2_WHEAT	P32032 triticum ae
5	214	82.6	136	1	THNB_WHEAT	P01543 triticum ae
6	166.5	64.3	137	1	THN6_HORVU	P09618 hordeum vul
7	161.5	62.4	137	1	THN3_HORVU	P08772 hordeum vul
8	146	56.4	47	1	THN_PYRPU	P07504 pyrularia p
9	145.5	56.2	137	1	THN5_HORVU	P09617 hordeum vul
10	129.5	50.0	111	1	THN3_VISAL	P01538 viscum albu
11	128.5	49.6	103	1	THNB_VISAL	P08943 viscum albu
12	116.5	45.0	46	1	THNB_PHOLI	P59358 phoradendro
13	115.5	44.6	46	1	THN2_VISAL	P32880 viscum albu
14	113.5	43.8	46	1	THN_DENCL	P01541 dendrophtho
15	109.5	42.3	46	1	THNA_PHOLI	P01540 phoradendro
16	108.5	41.9	46	1	THN1_VISAL	P01537 viscum albu
17	108.5	41.9	46	1	THN_PHOTO	P01539 phoradendro
18	75.5	29.2	46	1	CRAM_CRAAB	P01542 crambe abys
19	70.5	27.2	1786	1	LMB1_HUMAN	P07942 homo sapien
20	69.5	26.8	1786	1	LMB1_MOUSE	P02469 mus musculu
21	67.5	26.1	1328	1	AGRI_DISOM	Q90404 discopyge o
22	64.5	24.9	72	1	MT1A_MYTED	P80246 mytilus edu
23	64.5	24.9	72	1	MT1B_MYTED	O62554 mytilus edu
24	64	24.7	739	1	AD18_HUMAN	Q9y3q7 homo sapien
25	63	24.3	71	1	MT21_MYTED	P80251 mytilus edu
26	62.5	24.1	72	1	MT12_MYTED	P80247 mytilus edu
27	62.5	24.1	349	1	CTGF_HUMAN	P29279 homo sapien
28	62	23.9	845	1	ITBX_DROME	P11584 drosophila
29	61	23.6	746	1	AD18_MACFA	Q95194 macaca fasc
30	61	23.6	870	1	SRC2_HUMAN	Q96gp6 homo sapien
31	60.5	23.4	61	1	MT1B_HUMAN	P07438 homo sapien
32	60.5	23.4	63	1	MT2_COLLI	P15787 columba liv
33	60	23.2	71	1	MT22_MYTED	P80252 mytilus edu
34	60	23.2	727	1	NETA_DROME	Q24567 drosophila
35	59.5	23.0	58	1	CTC7_HUMAN	Q9bqn2 homo sapien
36	58.5	22.6	72	1	MT13_MYTED	P80248 mytilus edu
37	58.5	22.6	72	1	MT14_MYTED	P80249 mytilus edu
38	58.5	22.6	98	1	SRG1_MOUSE	O88745 mus musculu
39	58.5	22.6	98	1	SRG1_RAT	Q9z0k6 rattus norv
40	58.5	22.6	830	1	SREC_HUMAN	Q14162 homo sapien
41	58.5	22.6	3075	1	LMA1_HUMAN	P25391 homo sapien
42	58	22.4	288	1	SPY3_HUMAN	O43610 homo sapien
43	58	22.4	612	1	UNC6_CAEEL	P34710 caenorhabdi
44	58	22.4	719	1	AD18_MOUSE	Q9r157 mus musculu
45	57.5	22.2	61	1	MT2_BOVIN	P09579 bos taurus

ALIGNMENTS

```
RESULT 1
THNA_HORVU
ID   THNA_HORVU     STANDARD;      PRT;   127 AA.
AC   P01545;
DT   21-JUL-1986 (Rel. 01, Created)
DT   23-OCT-1986 (Rel. 02, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Alpha-hordothionin precursor (Purothionin II).
GN   THI1.1.
OS   Hordeum vulgare (Barley).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Triticeae; Hordeum.
OX   NCBI_TaxID=4513;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86164332; PubMed=3082629;
RA   Ponz F., Paz-Ares J., Hernandez-Lucas C., Garcia-Olmedo F.,
RA   Carbonero P.;
RT   "Cloning and nucleotide sequence of a cDNA encoding the precursor of
RT   the barley toxin alpha-hordothionin.";
RL   Eur. J. Biochem. 156:131-135(1986).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89108011; PubMed=2850969;
RA   Rodriguez-Palenzuela P., Pintor-Toro J.A., Carbonero P.,
RA   Garcia-Olmedo F.;
RT   "Nucleotide sequence and endosperm-specific expression of the
RT   structural gene for the toxin alpha-hordothionin in barley (Hordeum
RT   vulgare L.).";
RL   Gene 70:271-281(1988).
RN   [3]
RP   SEQUENCE OF 19-63.
RX   MEDLINE=80137408; PubMed=6987216;
RA   Ozaki Y., Wada K., Hase T., Matsubara H., Nakanishi T., Yoshizumi H.;
RT   "Amino acid sequence of a purothionin homolog from barley flour.";
RL   J. Biochem. 87:549-555(1980).
RN   [4]
RP   SEQUENCE OF 19-27.
RC   STRAIN=cv. Bomi; TISSUE=Starchy endosperm;
RX   MEDLINE=21088911; PubMed=11271488;
RA   Kristoffersen H.E., Flengsrud R.;
RT   "Separation and characterization of basic barley seed proteins.";
RL   Electrophoresis 21:3693-3700(2000).
CC   -!- FUNCTION: THIONINS ARE SMALL PLANT PROTEINS WHICH ARE TOXIC
CC       TO ANIMAL CELLS. THEY SEEM TO EXERT THEIR TOXIC EFFECT AT THE
CC       LEVEL OF THE CELL MEMBRANE. THE PRECISE FUNCTION, IN PLANTS,
CC       OF THESE PROTEINS IS NOT KNOWN.
CC   -!- SIMILARITY: BELONGS TO THE PLANT THIONIN FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
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CC   or send an email to license@isb-sib.ch).
CC   ------------------------------------------------------------------------
DR   EMBL; X05901; CAA29330.1; -.
DR   EMBL; M23080; AAA32966.1; ALT_INIT.
DR   PIR; JA0087; VSBH2.
DR   HSSP; P01544; 2PLH.
DR   InterPro; IPR001010; Thionin.
DR   Pfam; PF00321; plant_thionins; 1.
DR   PROSITE; PS00271; THIONIN; 1.
KW   Thionin; Plant toxin; Signal; Multigene family.
FT   SIGNAL        1     18
FT   CHAIN        19     63       ALPHA-HORDOTHIONIN.
FT   CHAIN        64    127       ACIDIC PROTEIN.
FT   DISULFID     21     57
FT   DISULFID     22     49
FT   DISULFID     30     47
FT   DISULFID     34     43
SQ   SEQUENCE   127 AA;  13597 MW;  70C1BD787A9D1C46 CRC64;

  Query Match             100.0%;  Score 259;  DB 1;  Length 127;
  Best Local Similarity   100.0%;  Pred. No. 9.2e-24;
  Matches   45;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              |||||||||||||||||||||||||||||||||||||||||||||
Db         19 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 63


RESULT 2
THNB_HORVU
ID   THNB_HORVU     STANDARD;      PRT;   136 AA.
AC   P21742;
DT   01-MAY-1991 (Rel. 18, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Beta-hordothionin precursor.
GN   THI1.2.
OS   Hordeum vulgare (Barley).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Triticeae; Hordeum.
OX   NCBI_TaxID=4513;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Bomi; TISSUE=Endosperm;
RA   Rasmussen S.K., Rasmussen C.E.;
RT   "Full-length cDNA clone encoding barley toxin beta-hordothionin.";
RL   Plant Mol. Biol. 21:579-579(1993).
RN   [2]
RP   SEQUENCE OF 10-136 FROM N.A.
RA   Hernandez-Lucas C., Royo J., Paz-Ares J., Ponz F., Garcia-Olmedo F.,
RA   Carbonero P.;
RT   "Polyadenylation site heterogeneity in mRNA encoding the precursor of
RT   the barley toxin beta-hordothionin.";
RL   FEBS Lett. 200:103-106(1986).
CC   -!- FUNCTION: THIONINS ARE SMALL PLANT PROTEINS WHICH ARE TOXIC
CC       TO ANIMAL CELLS. THEY SEEM TO EXERT THEIR TOXIC EFFECT AT THE
CC       LEVEL OF THE CELL MEMBRANE. THE PRECISE FUNCTION, IN PLANTS,
CC       OF THESE PROTEINS IS NOT KNOWN.
CC   -!- SIMILARITY: BELONGS TO THE PLANT THIONIN FAMILY.
CC   ------------------------------------------------------------------------
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CC   ------------------------------------------------------------------------
DR   EMBL; Z13008; CAA78352.1; -.
DR   PIR; S22977; S22977.
DR   HSSP; P01543; 1BHP.
DR   InterPro; IPR001010; Thionin.
DR   Pfam; PF00321; plant_thionins; 1.
DR   PROSITE; PS00271; THIONIN; 1.
KW   Plant defense; Thionin; Plant toxin; Signal; Multigene family.
FT   SIGNAL        1     27
FT   CHAIN        28     72       BETA-HORDOTHIONIN.
FT   CHAIN        73    136       ACIDIC PROTEIN.
FT   DISULFID     30     66       BY SIMILARITY.
FT   DISULFID     31     58       BY SIMILARITY.
FT   DISULFID     39     56       BY SIMILARITY.
FT   DISULFID     43     52       BY SIMILARITY.
SQ   SEQUENCE   136 AA;  14603 MW;  F9E04874D44CF831 CRC64;

  Query Match             86.9%;  Score 225;  DB 1;  Length 136;
  Best Local Similarity   86.7%;  Pred. No. 9.1e-20;
  Matches   39;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              |||||||||||||||||||||||||  |||||||  ||| ||||
Db         28 KSCCRSTLGRNCYNLCRVRGAQKLCANACRCKLTSGLKCPSSFPK 72


RESULT 3
THN1_WHEAT
ID   THN1_WHEAT     STANDARD;      PRT;   126 AA.
AC   P01544;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Alpha-1-purothionin precursor (Purothionin A-II) (Fragment).
GN   THI1.1 OR PUR-D1.
OS   Triticum aestivum (Wheat).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Triticeae; Triticum.
OX   NCBI_TaxID=4565;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Endosperm;
RX   MEDLINE=95125120; PubMed=7824649;
RA   Castagnaro A., Marana C., Carbonero P., Garcia-Olmedo F.;
RT   "cDNA cloning and nucleotide sequences of alpha 1 and alpha 2
RT   thionins from hexaploid wheat endosperm.";
RL   Plant Physiol. 106:1221-1222(1994).
RN   [2]
RP   SEQUENCE OF 17-61.
RC   STRAIN=cv. Manitoba 3;
RX   MEDLINE=78026451; PubMed=914810;
RA   Ohtani S., Okada T., Yoshizumi H., Kagamiyama H.;
RT   "Complete primary structures of two subunits of purothionin A, a
RT   lethal protein for brewer's yeast from wheat flour.";
RL   J. Biochem. 82:753-767(1977).
RN   [3]
RP   SEQUENCE OF 17-61.
RA   Ohtani S., Okada T., Kagamiyama H., Yoshizumi H.;
RT   "The amino acid sequence of purothionin A, a lethal toxic protein
RT   to brewer's yeast from wheat.";
RL   Agric. Biol. Chem. 39:2269-2270(1975).
RN   [4]
RP   SEQUENCE OF 17-61.
RC   STRAIN=cv. Manitou;
RA   Jones B.L., Mak A.S.;
RT   "Amino acid sequences of the two alpha-purothionins of hexaploid
RT   wheat.";
RL   Cereal Chem. 54:511-523(1977).
RN   [5]
RP   X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX   MEDLINE=91045879; PubMed=2235992;
RA   Teeter M.M., Ma X.-Q., Rao U., Whitlow M.;
RT   "Crystal structure of a protein-toxin alpha 1-purothionin at 2.5A and
RT   a comparison with predicted models.";
RL   Proteins 8:118-132(1990).
CC   -!- FUNCTION: THIONINS ARE SMALL PLANT PROTEINS WHICH ARE TOXIC
CC       TO ANIMAL CELLS. THEY SEEM TO EXERT THEIR TOXIC EFFECT AT THE
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CC       LEVEL OF THE CELL MEMBRANE. THE PRECISE FUNCTION, IN PLANTS,
CC       OF THESE PROTEINS IS NOT KNOWN.
CC   -!- SIMILARITY: BELONGS TO THE PLANT THIONIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X70666; CAA50004.1; -.
DR   PDB; 2PLH; 03-APR-96.
DR   InterPro; IPR001010; Thionin.
DR   Pfam; PF00321; plant_thionins; 1.
DR   PROSITE; PS00271; THIONIN; 1.
KW   Thionin; Plant toxin; Signal; 3D-structure.
FT   NON_TER       1      1
FT   SIGNAL       <1     16
FT   CHAIN        17     61       ALPHA-1-PUROTHIONIN.
FT   CHAIN        62    126       ACIDIC PROTEIN.
FT   DISULFID     19     55
FT   DISULFID     20     47
FT   DISULFID     28     45
FT   DISULFID     32     41
FT   STRAND       18     20
FT   HELIX        23     32
FT   TURN         33     35
FT   HELIX        38     45
FT   TURN         46     46
FT   STRAND       47     49
SQ   SEQUENCE   126 AA;  13525 MW;  FF7310D921C4EE30 CRC64;

; Query Match             86.5%;  Score 224;  DB 1;  Length 126;
  Best Local Similarity   84.4%;  Pred. No. 1.1e-19;
  Matches   38;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              |||||||||||||||| ||||||||||||::|   || ||||
Db         17 KSCCRSTLGRNCYNLCRARGAQKLCAGVCRCKISSGLSCPKGFPK 61


RESULT 4
THN2_WHEAT
ID   THN2_WHEAT     STANDARD;      PRT;   136 AA.
AC   P32032;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   Alpha-2-purothionin precursor.
GN   THI1.2 OR PUR-B1.
OS   Triticum aestivum (Wheat).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Triticeae; Triticum.
OX   NCBI_TaxID=4565;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Endosperm;
RX   MEDLINE=95125120; PubMed=7824649;
RA   Castagnaro A., Marana C., Carbonero P., Garcia-Olmedo F.;
RT   "cDNA cloning and nucleotide sequences of alpha 1 and alpha 2
RT   thionins from hexaploid wheat endosperm.";
RL   Plant Physiol. 106:1221-1222(1994).
CC   -!- FUNCTION: THIONINS ARE SMALL PLANT PROTEINS WHICH ARE TOXIC
CC       TO ANIMAL CELLS. THEY SEEM TO EXERT THEIR TOXIC EFFECT AT THE
CC       LEVEL OF THE CELL MEMBRANE. THE PRECISE FUNCTION, IN PLANTS,
CC       OF THESE PROTEINS IS NOT KNOWN.
CC   -!- SIMILARITY: BELONGS TO THE PLANT THIONIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X70665; CAA50003.1; -.
DR   PIR; S31695; S31695.
DR   HSSP; P01543; 1BHP.
DR   InterPro; IPR001010; Thionin.
DR   Pfam; PF00321; plant_thionins; 1.
DR   PROSITE; PS00271; THIONIN; 1.
KW   Thionin; Plant toxin; Signal.
FT   SIGNAL        1     27
FT   CHAIN        28     72       ALPHA-2-PUROTHIONIN.
FT   CHAIN        73    136       ACIDIC PROTEIN.
FT   DISULFID     30     66       BY SIMILARITY.
FT   DISULFID     31     58       BY SIMILARITY.
FT   DISULFID     39     56       BY SIMILARITY.
FT   DISULFID     43     52       BY SIMILARITY.
SQ   SEQUENCE   136 AA;  14558 MW;  B4019F014E226B9F CRC64;

  Query Match             82.6%;  Score 214;  DB 1;  Length 136;
  Best Local Similarity   82.2%;  Pred. No. 1.8e-18;
  Matches   37;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              |||||:|||||||||||| |||||||: ||||||||   || ||||
Db         28 KSCCRTTLGRNCYNLCRSRGAQKLCSTVCRCKLTSGLSCPKGFPK 72


RESULT 5
THNB_WHEAT
ID   THNB_WHEAT     STANDARD;      PRT;   136 AA.
AC   P01543;
DT   21-JUL-1986 (Rel. 01, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Purothionin A-I precursor (Beta-purothionin).
GN   THI1.3.
OS   Triticum aestivum (Wheat).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Triticeae; Triticum.
OX   NCBI_TaxID=4565;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Rosella;
RA   Hughes P.A., Llewellyn D.L., Whitecross M.;
RL   Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 28-72.
RC   STRAIN=cv. Manitoba 3;
RX   MEDLINE=78026451; PubMed=914810;
RA   Ohtani S., Okada T., Yoshizumi H., Kagamiyama H.;
RT   "Complete primary structures of two subunits of purothionin A, a
RT   lethal protein for brewer's yeast from wheat flour.";
RL   J. Biochem. 82:753-767(1977).
RN   [3]
RP   SEQUENCE OF 28-72.
RA   Ohtani S., Okada T., Kagamiyama H., Yoshizumi H.;
RT   "The amino acid sequence of purothionin A, a lethal toxic protein
RT   to brewer's yeast from wheat.";
RL   Agric. Biol. Chem. 39:2269-2270(1975).
RN   [4]
RP   SEQUENCE OF 28-72.
RX   MEDLINE=77046666; PubMed=990986;
RA   Mak A.S., Jones B.L.;
RT   "The amino acid sequence of wheat beta-purothionin.";
RL   Can. J. Biochem. 54:835-842(1976).
RN   [5]
RP   X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
RA   Stec B., Rao U., Teeter M.M.;
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RT   "Refinement of purothionins reveals solute particles important for
RT   lattice formation and toxicity. Part 2: structure of beta-purothionin
RT   at 1.7-A resolution.";
RL   Acta Crystallogr. D 51:914-924(1995).
CC   -!- FUNCTION: THIONINS ARE SMALL PLANT PROTEINS WHICH ARE TOXIC
CC       TO ANIMAL CELLS. THEY SEEM TO EXERT THEIR TOXIC EFFECT AT THE
CC       LEVEL OF THE CELL MEMBRANE. THE PRECISE FUNCTION, IN PLANTS,
CC       OF THESE PROTEINS IS NOT KNOWN.
CC   -!- SIMILARITY: BELONGS TO THE PLANT THIONIN FAMILY.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF004018; AAB71137.1; -.
DR   PDB; 1BHP; 15-MAR-96.
DR   InterPro; IPR001010; Thionin.
DR   Pfam; PF00321; plant_thionins; 1.
DR   PROSITE; PS00271; THIONIN; 1.
KW   Thionin; Plant toxin; Signal; 3D-structure.
FT   SIGNAL        1     27
FT   CHAIN        28     72       PUROTHIONIN A-I.
FT   CHAIN        73    136       ACIDIC PROTEIN.
FT   DISULFID     30     66
FT   DISULFID     31     58
FT   DISULFID     39     56
FT   DISULFID     43     52
FT   STRAND       29     31
FT   HELIX        34     43
FT   TURN         44     46
FT   HELIX        49     55
FT   TURN         56     57
FT   STRAND       58     60
FT   TURN         68     69
SQ   SEQUENCE   136 AA;  14625 MW;  A855C815519EDA24 CRC64;

  Query Match             82.6%;  Score 214;  DB 1;  Length 136;
  Best Local Similarity   82.2%;  Pred. No. 1.8e-18;
  Matches   37;  Conservative    1;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              ||||:|||||||||||| |||||||| ||||||||   ||  |||
Db         28 KSCCKSTLGRNCYNLCRARGAQKLCANVCRCKLTSGLSCPKDFPK 72


RESULT 6
THN6_HORVU
ID   THN6_HORVU     STANDARD;      PRT;   137 AA.
AC   P09618;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Leaf-specific thionin precursor (Clone BTH6).
OS   Hordeum vulgare (Barley).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Triticeae; Hordeum.
OX   NCBI_TaxID=4513;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Holtorf S., Schuetz C., Apel K., Bohlmann H.;
RL   Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 29-74 FROM N.A.
RC   STRAIN=cv. Carina;
RA   Bohlmann H., Clausen S., Behnke S., Giese H., Hiller C.,
RA   Reimann-Phillip U., Schrader G., Barkholt V., Apel K.;
RT   "Leaf-specific thionins of barley - a novel class of cell wall
RT   proteins toxic to plant-pathogenic fungi and possibly involved in the
RT   defence mechanism of plants.";
RL   EMBO J. 7:1559-1565(1988).
CC   -!- FUNCTION: THIONINS ARE SMALL PLANT PROTEINS WHICH ARE TOXIC
CC       TO ANIMAL CELLS. THEY SEEM TO EXERT THEIR TOXIC EFFECT AT THE
CC       LEVEL OF THE CELL MEMBRANE. THE PRECISE FUNCTION, IN PLANTS,
CC       OF THESE PROTEINS IS NOT KNOWN.
CC   -!- SIMILARITY: BELONGS TO THE PLANT THIONIN FAMILY.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L36882; AAA91047.1; -.
DR   HSSP; P01543; 1BHP.
DR   InterPro; IPR001010; Thionin.
DR   Pfam; PF00321; plant_thionins; 1.
DR   PROSITE; PS00271; THIONIN; 1.
KW   Plant defense; Thionin; Plant toxin; Multigene family; Signal.
FT   SIGNAL        1     28       BY SIMILARITY.
FT   CHAIN        29     74       LEAF-SPECIFIC THIONIN.
FT   CHAIN        75    137       ACIDIC PROTEIN.
FT   DISULFID     31     68       BY SIMILARITY.
FT   DISULFID     32     60       BY SIMILARITY.
FT   DISULFID     40     58       BY SIMILARITY.
FT   DISULFID     44     54       BY SIMILARITY.
SQ   SEQUENCE   137 AA;  14717 MW;  559302CCCB34364A CRC64;

  Query Match             64.3%;  Score 166.5;  DB 1;  Length 137;
  Best Local Similarity   58.7%;  Pred. No. 6.3e-13;
  Matches   27;  Conservative    6;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQK-LCAGVCRCKLTSSGKCPTGFPK 45
              ||||: || ||||| ||  |  : :||| ||||: |  |||: :||
Db         29 KSCCKDTLARNCYNTCRFAGGSRPVCAGACRCKIISGPKCPSDYPK 74


RESULT 7
THN3_HORVU
ID   THN3_HORVU     STANDARD;      PRT;   137 AA.
AC   P08772;
DT   01-NOV-1988 (Rel. 09, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Leaf-specific thionin precursor (Clone DB4).
GN   THI1.3.
OS   Hordeum vulgare (Barley).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Triticeae; Hordeum.
OX   NCBI_TaxID=4513;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Carina;
RA   Bohlmann H., Apel K.;
RT   "Isolation and characterization of cDNAs coding for leaf-specific
RT   thionins closely related to the endosperm-specific hordothionin of
RT   barley (Hordeum vulgare L.).";
RL   Mol. Gen. Genet. 207:446-454(1987).
CC   -!- FUNCTION: THIONINS ARE SMALL PLANT PROTEINS WHICH ARE TOXIC
CC       TO ANIMAL CELLS. THEY SEEM TO EXERT THEIR TOXIC EFFECT AT THE
CC       LEVEL OF THE CELL MEMBRANE. THE PRECISE FUNCTION, IN PLANTS,
CC       OF THESE PROTEINS IS NOT KNOWN.
CC   -!- SIMILARITY: BELONGS TO THE PLANT THIONIN FAMILY.
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CC   ----------------------------------------------------------------------------
DR   EMBL; X05576; CAA29082.1; -.
DR   PIR; S07648; S07648.
DR   HSSP; P01543; 1BHP.
DR   InterPro; IPR001010; Thionin.
DR   Pfam; PF00321; plant_thionins; 1.
DR   PROSITE; PS00271; THIONIN; 1.
KW   Plant defense; Thionin; Plant toxin; Signal; Multigene family.
FT   SIGNAL        1     28
FT   CHAIN        29     74       LEAF-SPECIFIC THIONIN.
FT   CHAIN        75    137       ACIDIC PROTEIN.
FT   DISULFID     31     68       BY SIMILARITY.
FT   DISULFID     32     60       BY SIMILARITY.
FT   DISULFID     40     58       BY SIMILARITY.
FT   DISULFID     44     54       BY SIMILARITY.
SQ   SEQUENCE   137 AA;  14711 MW;  5E76AECB4EE12DE7 CRC64;

  Query Match             62.4%;  Score 161.5;  DB 1;  Length 137;
  Best Local Similarity   56.5%;  Pred. No. 2.4e-12;
  Matches   26;  Conservative    6;  Mismatches   13;  Indels    1;  Gaps    1;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQK-LCAGVCRCKLTSSGKCPTGFPK 45
              |||| || ||||| |   |  : :||| ||||: |  |||: :||
Db         29 KSCCKDTLARNCYNTCHFAGGSRPVCAGACRCKIISGPKCPSDYPK 74


RESULT 8
THN_PYRPU
ID   THN_PYRPU      STANDARD;      PRT;    47 AA.
AC   P07504;
DT   01-APR-1988 (Rel. 07, Created)
DT   01-APR-1988 (Rel. 07, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Thionin.
GN   THI1.
OS   Pyrularia pubera (Rabbitwood) (Buffalo nut).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Santalales; Santalaceae; Pyrularia.
OX   NCBI_TaxID=3960;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=85173323; PubMed=3985614;
RA   Vernon L.P., Evett G.E., Zeikus R.D., Gray W.R.;
RT   "A toxic thionin from Pyrularia pubera: purification, properties, and
RT   amino acid sequence.";
RL   Arch. Biochem. Biophys. 238:18-29(1985).
CC   -!- FUNCTION: THIONINS ARE SMALL PLANT PROTEINS WHICH ARE TOXIC
CC       TO ANIMAL CELLS. THEY SEEM TO EXERT THEIR TOXIC EFFECT AT THE
CC       LEVEL OF THE CELL MEMBRANE. THE PRECISE FUNCTION, IN PLANTS,
CC       OF THESE PROTEINS IS NOT KNOWN.
CC   -!- SIMILARITY: BELONGS TO THE PLANT THIONIN FAMILY.
DR   PIR; A24074; A24074.
DR   HSSP; P01544; 2PLH.
DR   InterPro; IPR001010; Thionin.
DR   Pfam; PF00321; plant_thionins; 1.
DR   PROSITE; PS00271; THIONIN; 1.
KW   Plant defense; Thionin; Plant toxin.
FT   DISULFID      3     41       BY SIMILARITY.
FT   DISULFID      4     31       BY SIMILARITY.
FT   DISULFID     16     27       BY SIMILARITY.
SQ   SEQUENCE   47 AA;  5288 MW;  87E10460D8E4C6E1 CRC64;

  Query Match             56.4%;  Score 146;  DB 1;  Length 47;
  Best Local Similarity   51.1%;  Pred. No. 6.2e-11;
  Matches   24;  Conservative   10;  Mismatches   11;  Indels    2;  Gaps    1;

Qy          1 KSCCRSTLGRNCYNLCRVRG--AQKLCAGVCRCKLTSSGKCPTGFPK 45
              |||||:|  |||||:||: |  ::::||  | ||: |   ||: :||
Db          1 KSCCRNTWARNCYNVCRLPGTISREICAKKCDCKIISGTTCPSDYPK 47


RESULT 9
THN5_HORVU
ID   THN5_HORVU     STANDARD;      PRT;   137 AA.
AC   P09617;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Leaf-specific thionin precursor (Clones PKG1348, PKG1940, PKG2872 and
DE   DG3).
GN   THI1.5.
OS   Hordeum vulgare (Barley).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Triticeae; Hordeum.
OX   NCBI_TaxID=4513;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Gausing K.;
RT   "Thionin genes specifically expressed in barley leaves.";
RL   Planta 171:241-246(1987).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Carina;
RX   MEDLINE=92322947; PubMed=1377959;
RA   Andresen I., Becker W., Schluter K., Burges J., Parthier B.,
RA   Apel K.;
RT   "The identification of leaf thionin as one of the main
RT   jasmonate-induced proteins of barley (Hordeum vulgare).";
RL   Plant Mol. Biol. 19:193-204(1992).
RN   [3]
RP   SEQUENCE OF 29-74 FROM N.A. (CLONE DG3).
RC   STRAIN=cv. Carina;
RA   Bohlmann H., Clausen S., Behnke S., Giese H., Hiller C.,
RA   Reimann-Phillip U., Schrader G., Barkholt V., Apel K.;
RT   "Leaf-specific thionins of barley - a novel class of cell wall
RT   proteins toxic to plant-pathogenic fungi and possibly involved in the
RT   defence mechanism of plants.";
RL   EMBO J. 7:1559-1565(1988).
CC   -!- FUNCTION: THIONINS ARE SMALL PLANT PROTEINS WHICH ARE TOXIC
CC       TO ANIMAL CELLS. THEY SEEM TO EXERT THEIR TOXIC EFFECT AT THE
CC       LEVEL OF THE CELL MEMBRANE. THE PRECISE FUNCTION, IN PLANTS,
CC       OF THESE PROTEINS IS NOT KNOWN.
CC   -!- SIMILARITY: BELONGS TO THE PLANT THIONIN FAMILY.
CC   ----------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------------
DR   EMBL; M19046; AAA32976.1; -.
DR   EMBL; M19047; AAA32977.1; -.
DR   EMBL; M19048; AAA32978.1; -.
DR   PIR; S22515; S22515.
DR   HSSP; P01543; 1BHP.
DR   InterPro; IPR001010; Thionin.
DR   Pfam; PF00321; plant_thionins; 1.
DR   PROSITE; PS00271; THIONIN; 1.
KW   Plant defense; Thionin; Plant toxin; Signal; Multigene family.
FT   SIGNAL        1     28
FT   CHAIN        29     74       LEAF-SPECIFIC THIONIN.
FT   CHAIN        75    137       ACIDIC PROTEIN.
FT   DISULFID     31     68       BY SIMILARITY.
FT   DISULFID     32     60       BY SIMILARITY.
FT   DISULFID     40     58       BY SIMILARITY.
FT   DISULFID     44     54       BY SIMILARITY.
FT   VARIANT      28     28       A -> G (IN REF. 2).
FT   VARIANT     135    135       V -> L (IN REF. 2).
SQ   SEQUENCE   137 AA;  14662 MW;  FD00C2DBF6632797 CRC64;
```

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  Query Match             56.2%;  Score 145.5;  DB 1;  Length 137;
  Best Local Similarity   52.2%;  Pred. No. 1.8e-10;
  Matches   24;  Conservative    6;  Mismatches   15;  Indels    1;  Gaps    1;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQK-LCAGVCRCKLTSSGKCPTGFPK 45
              ||||::| |||||| ||  |  : :||  | ||: |   ||  :||
Db         29 KSCCKNTTGRNCYNACRFAGGSRPVCATACGCKIISGPTCPRDYPK 74


RESULT 10
THN3_VISAL
ID   THN3_VISAL     STANDARD;      PRT;   111 AA.
AC   P01538;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Viscotoxin A3 precursor.
GN   THI2.1.
OS   Viscum album (European mistletoe).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Santalales; Santalaceae; Viscum.
OX   NCBI_TaxID=3972;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91266934; PubMed=1710983;
RA   Schrader G., Apel K.;
RT   "Isolation and characterization of cDNAs encoding viscotoxins of
RT   mistletoe (Viscum album).";
RL   Eur. J. Biochem. 198:549-553(1991).
RN   [2]
RP   SEQUENCE OF 27-72.
RX   MEDLINE=69157811; PubMed=5719166;
RA   Samuelsson G., Seger L., Olson T.;
RT   "The amino acid sequence of oxidized viscotoxin A3 from the European
RT   mistletoe (Viscum album L, Loranthaceae).";
RL   Acta Chem. Scand. 22:2624-2642(1968).
RN   [3]
RP   DISULFIDE BONDS.
RX   MEDLINE=72049894; PubMed=4941626;
RA   Samuelsson G., Pettersson B.;
RT   "The disulfide bonds of viscotoxin A3 from the European mistletoe
RT   (Viscum album L., Loranthaceae).";
RL   Acta Chem. Scand. 25:2048-2054(1971).
CC   -!- FUNCTION: THIONINS ARE SMALL PLANT PROTEINS WHICH ARE TOXIC
CC       TO ANIMAL CELLS. THEY SEEM TO EXERT THEIR TOXIC EFFECT AT THE
CC       LEVEL OF THE CELL MEMBRANE. THE PRECISE FUNCTION, IN PLANTS,
CC       OF THESE PROTEINS IS NOT KNOWN.
CC   -!- SIMILARITY: BELONGS TO THE PLANT THIONIN FAMILY.
DR   PDB; 1ED0; 04-FEB-00.
DR   InterPro; IPR001010; Thionin.
DR   Pfam; PF00321; plant_thionins; 1.
DR   PROSITE; PS00271; THIONIN; 1.
KW   Plant defense; Signal; Thionin; Plant toxin; 3D-structure.
FT   SIGNAL        1     26
FT   CHAIN        27     72       VISCOTOXIN A3.
FT   CHAIN        73    111       ACIDIC PROTEIN.
FT   DISULFID     29     66
FT   DISULFID     30     58
FT   DISULFID     42     52
FT   CONFLICT     69     71       DYP -> YPD (IN REF. 2).
SQ   SEQUENCE   111 AA;  11620 MW;  749F7D70CA0BDF96 CRC64;

  Query Match             50.0%;  Score 129.5;  DB 1;  Length 111;
  Best Local Similarity   50.0%;  Pred. No. 1.1e-08;
  Matches   23;  Conservative    7;  Mismatches   15;  Indels    1;  Gaps    1;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQK-LCAGVCRCKLTSSGKCPTGFPK 45
              |||| :| ||| || ||: || :  || :  ||: |   ||: :||
Db         27 KSCCPNTTGRNIYNACRLTGAPRPTCAKLSGCKIISGSTCPSDYPK 72


RESULT 11
THNB_VISAL
ID   THNB_VISAL     STANDARD;      PRT;   103 AA.
AC   P08943; P01536;
DT   01-NOV-1988 (Rel. 09, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Viscotoxin B precursor (Fragment).
GN   THI2.2.
OS   Viscum album (European mistletoe).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Santalales; Santalaceae; Viscum.
OX   NCBI_TaxID=3972;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91266934; PubMed=1710983;
RA   Schrader G., Apel K.;
RT   "Isolation and characterization of cDNAs encoding viscotoxins of
RT   mistletoe (Viscum album).";
RL   Eur. J. Biochem. 198:549-553(1991).
RN   [2]
RP   SEQUENCE OF 7-52.
RX   MEDLINE=71284202; PubMed=5568678;
RA   Samuelsson G., Pettersson B.M.;
RT   "The amino acid sequence of viscotoxin B from the European mistletoe
RT   (Viscum album L, loranthaceae).";
RL   Eur. J. Biochem. 21:86-89(1971).
CC   -!- FUNCTION: THIONINS ARE SMALL PLANT PROTEINS WHICH ARE TOXIC
CC       TO ANIMAL CELLS. THEY SEEM TO EXERT THEIR TOXIC EFFECT AT THE
CC       LEVEL OF THE CELL MEMBRANE. THE PRECISE FUNCTION, IN PLANTS,
CC       OF THESE PROTEINS IS NOT KNOWN.
CC   -!- SIMILARITY: BELONGS TO THE PLANT THIONIN FAMILY.
DR   PIR; A91187; VTVAB.
DR   HSSP; P01543; 1BHP.
DR   InterPro; IPR001010; Thionin.
DR   Pfam; PF00321; plant_thionins; 1.
DR   PROSITE; PS00271; THIONIN; 1.
KW   Plant defense; Thionin; Plant toxin; Signal.
FT   NON_TER       1      1
FT   SIGNAL       <1      6
FT   CHAIN         7     52       VISCOTOXIN B.
FT   PROPEP       53     72
FT   CHAIN        73    103       ACIDIC PROTEIN.
FT   DISULFID      9     46       BY SIMILARITY.
FT   DISULFID     10     38       BY SIMILARITY.
FT   DISULFID     22     32       BY SIMILARITY.
FT   CONFLICT     49     51       DYP -> YPD (IN REF. 2).
SQ   SEQUENCE   103 AA;  11008 MW;  99E3DD135FEE0846 CRC64;

  Query Match             49.6%;  Score 128.5;  DB 1;  Length 103;
  Best Local Similarity   47.8%;  Pred. No. 1.3e-08;
  Matches   22;  Conservative   10;  Mismatches   13;  Indels    1;  Gaps    1;

Qy          1 KSCCRSTLGRNCYNLCRV-RGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              |||| :| ||| || ||:  |::: || :  ||: |:  ||: :||
Db          7 KSCCPNTTGRNIYNTCRLGGGSRERCASLSGCKIISASTCPSDYPK 52


RESULT 12
THNB_PHOLI
ID   THNB_PHOLI     STANDARD;      PRT;    46 AA.
AC   P59358;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ligatoxin B.
OS   Phoradendron liga (Argentine mistletoe).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Santalales; Santalaceae; Phoradendron.
OX   NCBI_TaxID=3968;
RN   [1]
RP   SEQUENCE.
```

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RX   MEDLINE=22176324; PubMed=12049612;
RA   Li S.S., Gullbo J., Lindholm P., Larsson R., Thunberg E.,
RA   Samuelsson G., Bohlin L., Claeson P.;
RT   "Ligatoxin B, a new cytotoxic protein with a novel helix-turn-helix
RT   DNA-binding domain from the mistletoe Phoradendron liga.";
RL   Biochem. J. 366:405-413(2002).
CC   -!- FUNCTION: Thionins are small plant proteins which are toxic
CC       to animal cells. They seem to exert their toxic effect at the
CC       level of the cell membrane.
CC   -!- MISCELLANEOUS: The predicted 3D structure shares similarity with
CC       the HTH DNA-binding motifs, leading to the suggestion that the
CC       intracellular thionins of an infected plant may activate signaling
CC       networks that regulate innate responses, including the
CC       hypersensitive reaction.
CC   -!- SIMILARITY: BELONGS TO THE PLANT THIONIN FAMILY.
DR   Pfam; PF00321; plant_thionins; 1.
DR   PROSITE; PS00271; THIONIN; 1.
KW   Plant defense; Thionin; Plant toxin.
FT   DISULFID     3     40       BY SIMILARITY.
FT   DISULFID     4     32       BY SIMILARITY.
FT   DISULFID    16     26       BY SIMILARITY.
SQ   SEQUENCE   46 AA;  4798 MW;  A041A0C9F5A479D6 CRC64;

  Query Match             45.0%;  Score 116.5;  DB 1;  Length 46;
  Best Local Similarity   47.7%;  Pred. No. 1.7e-07;
  Matches   21;  Conservative    7;  Mismatches   15;  Indels    1;  Gaps    1;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQK-LCAGVCRCKLTSSGKCPTGF 43
              |||| ||  || || ||: || : :|| :  ||: |   | :|:
Db          1 KSCCPSTTARNIYNTCRLTGASRSVCASLSGCKIISGSTCDSGW 44


RESULT 13
THN2_VISAL
ID   THN2_VISAL     STANDARD;      PRT;    46 AA.
AC   P32880; P01536;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Viscotoxin A2.
GN   THI2.3.
OS   Viscum album (European mistletoe).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Santalales; Santalaceae; Viscum.
OX   NCBI_TaxID=3972;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=72211843; PubMed=5035954;
RA   Olson T., Samuelsson G.;
RT   "The amino acid sequence of viscotoxin A2 from the European mistletoe
RT   (Viscum album L., Loranthaceae).";
RL   Acta Chem. Scand. 26:585-595(1972).
RN   [2]
RP   DISULFIDE BONDS.
RX   MEDLINE=75015879; PubMed=4607177;
RA   Olson T., Samuelsson G.;
RT   "The disulphide bonds of viscotoxin A2 from the European mistletoe
RT   (Viscum album L. Loranthaceae).";
RL   Acta Pharm. Suec. 11:381-386(1974).
CC   -!- FUNCTION: THIONINS ARE SMALL PLANT PROTEINS WHICH ARE TOXIC
CC       TO ANIMAL CELLS. THEY SEEM TO EXERT THEIR TOXIC EFFECT AT THE
CC       LEVEL OF THE CELL MEMBRANE. THE PRECISE FUNCTION, IN PLANTS,
CC       OF THESE PROTEINS IS NOT KNOWN.
CC   -!- SIMILARITY: BELONGS TO THE PLANT THIONIN FAMILY.
DR   PIR; A90005; VTVAA2.
DR   HSSP; P01544; 2PLH.
DR   InterPro; IPR001010; Thionin.
DR   Pfam; PF00321; plant_thionins; 1.
DR   PROSITE; PS00271; THIONIN; 1.
KW   Plant defense; Thionin; Plant toxin.
FT   DISULFID     3     40       PROBABLE.
FT   DISULFID     4     32       PROBABLE.
FT   DISULFID    16     26
SQ   SEQUENCE   46 AA;  4834 MW;  61149207EE3FF0E5 CRC64;

  Query Match             44.6%;  Score 115.5;  DB 1;  Length 46;
  Best Local Similarity   47.6%;  Pred. No. 2.2e-07;
  Matches   20;  Conservative    9;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          1 KSCCRSTLGRNCYNLCRV-RGAQKLCAGVCRCKLTSSGKCPT 41
              |||| :| ||| || ||   |::::|| :  ||: |:  ||:
Db          1 KSCCPNTTGRNIYNTCRFGGGSREVCASLSGCKIISASTCPS 42


RESULT 14
THN_DENCL
ID   THN_DENCL      STANDARD;      PRT;    46 AA.
AC   P01541;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Denclatoxin B.
OS   Dendrophthora clavata (Columbian mistletoe).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Santalales; Santalaceae; Dendrophthora.
OX   NCBI_TaxID=3965;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=78016835; PubMed=906843;
RA   Samuelsson G., Pettersson B.;
RT   "Toxic proteins from the mistletoe Dendrophtora clavata. II. The
RT   amino acid sequence of denclatoxin B.";
RL   Acta Pharm. Suec. 14:245-254(1977).
CC   -!- FUNCTION: THIONINS ARE SMALL PLANT PROTEINS WHICH ARE TOXIC
CC       TO ANIMAL CELLS. THEY SEEM TO EXERT THEIR TOXIC EFFECT AT THE
CC       LEVEL OF THE CELL MEMBRANE. THE PRECISE FUNCTION, IN PLANTS,
CC       OF THESE PROTEINS IS NOT KNOWN.
CC   -!- SIMILARITY: BELONGS TO THE PLANT THIONIN FAMILY.
DR   PIR; A01804; DKDCB.
DR   HSSP; P01542; 1CBN.
DR   InterPro; IPR001010; Thionin.
DR   Pfam; PF00321; plant_thionins; 1.
DR   PROSITE; PS00271; THIONIN; 1.
KW   Plant defense; Thionin; Plant toxin.
FT   DISULFID     3     40       BY SIMILARITY.
FT   DISULFID     4     32       BY SIMILARITY.
FT   DISULFID    16     26       BY SIMILARITY.
SQ   SEQUENCE   46 AA;  4821 MW;  C107A82B29ADA608 CRC64;

  Query Match             43.8%;  Score 113.5;  DB 1;  Length 46;
  Best Local Similarity   45.5%;  Pred. No. 3.8e-07;
  Matches   20;  Conservative    8;  Mismatches   15;  Indels    1;  Gaps    1;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQK-LCAGVCRCKLTSSGKCPTGF 43
              |||| :|  || ||:||: |  : :|| :  ||: |   || |:
Db          1 KSCCPTTAARNQYNICRLPGTPRPVCAALSGCKIISGTGCPPGY 44


RESULT 15
THNA_PHOLI
ID   THNA_PHOLI     STANDARD;      PRT;    46 AA.
AC   P01540;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ligatoxin A.
OS   Phoradendron liga (Argentine mistletoe).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Santalales; Santalaceae; Phoradendron.
OX   NCBI_TaxID=3968;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=83044670; PubMed=7136736;
```

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RA   Thunberg E., Samuelsson G.;
RT   "Isolation and properties of ligatoxin A, a toxic protein from the
RT   mistletoe Phoradendron liga.";
RL   Acta Pharm. Suec. 19:285-292(1982).
CC   -!- FUNCTION: Thionins are small plant proteins which are toxic
CC       to animal cells. They seem to exert their toxic effect at the
CC       level of the cell membrane. The precise function, in plants,
CC       of these proteins is not known.
CC   -!- SIMILARITY: BELONGS TO THE PLANT THIONIN FAMILY.
DR   PIR; A01803; LOFDAL.
DR   HSSP; P01544; 2PLH.
DR   InterPro; IPR001010; Thionin.
DR   Pfam; PF00321; plant_thionins; 1.
DR   PROSITE; PS00271; THIONIN; 1.
KW   Plant defense; Thionin; Plant toxin.
FT   DISULFID     3     40       BY SIMILARITY.
FT   DISULFID     4     32       BY SIMILARITY.
FT   DISULFID    16     26       BY SIMILARITY.
SQ   SEQUENCE   46 AA;  4840 MW;  635EB18CF5A26D5B CRC64;

  Query Match             42.3%;  Score 109.5;  DB 1;  Length 46;
  Best Local Similarity   45.5%;  Pred. No. 1.1e-06;
  Matches   20;  Conservative    6;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQK-LCAGVCRCKLTSSGKCPTGF 43
              |||| ||  || || ||: |  :  || :  ||: |   | :|:
Db          1 KSCCPSTTARNIYNTCRLTGTSRPTCASLSGCKIISGSTCBSGW 44


Search completed: January 21, 2004, 09:46:19
Job time : 11 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 21, 2004, 09:45:17 ; Search time 21 Seconds
(without alignments)
206.076 Million cell updates/sec

Title: US-10-010-709-1
Perfect score: 259
Sequence: 1 KSCCRSTLGRNCYNLCRVRG.....AGVCRCKLTSSGKCPTGFPK 45

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	259	100.0	133	1	VSBH2	alpha-hordothionin
2	225	86.9	136	2	S22977	beta-hordothionin
3	224	86.5	125	1	VSWTA2	alpha-2-thionin -
4	214	82.6	45	1	VSWTA1	purothionin A-I -
5	214	82.6	136	2	S31695	alpha-1-thionin -
6	161.5	62.4	137	2	S07648	thionin precursor,
7	146	56.4	47	1	A24074	pyrularia thionin
8	145.5	56.2	137	2	S22515	thionin precursor,
9	129.5	50.0	111	2	S16099	viscotoxin - Europ
10	118.5	45.8	133	2	S52554	thionin variant Th
11	115.5	44.6	46	1	VTVAA2	viscotoxin A2 - Eu
12	115.5	44.6	46	1	VTVAA3	viscotoxin A3 - Eu
13	114.5	44.2	46	1	VTVAB	viscotoxin B - Eur
14	113.5	43.8	46	1	DKDCB	denclatoxin B - Co
15	109.5	42.3	46	1	LOFDAL	ligatoxin A - Arge
16	109.5	42.3	135	2	S52555	thionin variant Th
17	108.5	41.9	46	1	VTVA1P	viscotoxin 1-PS -
18	108.5	41.9	46	1	VFFD1T	phoratoxin - Calif
19	98.5	38.0	135	2	S52552	thionin variant Th
20	96.5	37.3	134	2	S52553	thionin variant Th
21	88.5	34.2	133	2	S52547	thionin variant Th
22	86	33.2	118	2	C96746	thionin, 63255-627
23	83.5	32.2	134	2	S52546	thionin variant Th
24	82.5	31.9	125	2	S52548	thionin variant Th
25	82.5	31.9	125	2	S52550	thionin variant Th
26	78.5	30.3	135	2	H84523	probable thionin [
27	76	29.3	1574	2	T13954	MEGF6 protein - ra
28	75.5	29.2	118	2	S52549	thionin variant Th
29	74.5	28.8	136	2	S52545	thionin variant Th
30	73.5	28.4	46	1	KECX	crambin - Abyssini
31	70.5	27.2	1786	1	MMHUB1	laminin beta-1 cha
32	69.5	26.8	1786	1	MMMSB1	laminin beta-1 cha
33	67.5	26.1	1328	2	T43060	agrin - electric r
34	66.5	25.7	1620	2	T27283	hypothetical prote
35	65.5	25.3	87	2	JQ1264	hypothetical 10K p
36	65.5	25.3	151	2	S60314	hair keratin cyste
37	64.5	24.9	72	2	S39416	metallothionein 10
38	63	24.3	71	2	S39420	metallothionein 20
39	63	24.3	358	2	T23802	hypothetical prote
40	62.5	24.1	72	2	S39417	metallothionein 10
41	62.5	24.1	349	2	A40551	connective tissue
42	62	23.9	71	2	S47576	metallothionein 20
43	62	23.9	846	2	A30889	integrin beta chai
44	61	23.6	1069	2	T42681	hypothetical prote
45	60.5	23.4	61	1	SMHU1B	metallothionein 1B

ALIGNMENTS

RESULT 1
VSBH2
alpha-hordothionin precursor - barley
N;Alternate names: purothionin II precursor; thionin
C;Species: Hordeum vulgare (barley)
C;Date: 31-May-1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
C;Accession: JA0087; A91164; A91956; A01808
R;Rodriguez-Palenzuela, P.; Pintor-Toro, J.A.; Carbonero, P.; Garcia-Olmedo, F.
Gene 70, 271-281, 1988
A;Title: Nucleotide sequence and endosperm-specific expression of the structural gene fo
A;Reference number: JA0087; MUID:89108011; PMID:2850969
A;Accession: JA0087
A;Molecule type: DNA
A;Residues: 1-133 <ROD>
A;Cross-references: GB:M23080; NID:g340805; PIDN:AAA32966.1; PID:g514332
A;Note: the authors translated the codon ATG for residue 93 as Asn
R;Ponz, F.; Paz-Ares, J.; Hernandez-Lucas, C.; Garcia-Olmedo, F.; Carbonero, P.
Eur. J. Biochem. 156, 131-135, 1986
A;Title: Cloning and nucleotide sequence of a cDNA encoding the precursor of the barley
A;Reference number: A91164; MUID:86164332; PMID:3082629
A;Accession: A91164
A;Molecule type: mRNA
A;Residues: 7-133 <PON>
A;Cross-references: GB:X05901; NID:g19109; PIDN:CAA29330.1; PID:g19110
R;Ozaki, Y.; Wada, K.; Hase, T.; Matsubara, H.; Nakanishi, T.; Yoshizumi, H.
J. Biochem. 87, 549-555, 1980
A;Title: Amino acid sequence of a purothionin homolog from barley flour.
A;Reference number: A91956; MUID:80137408; PMID:6987216
A;Accession: A91956
A;Molecule type: protein
A;Residues: 25-69 <OZA>
C;Genetics:
A;Introns: 77/1; 101/1
C;Superfamily: viscotoxin
C;Keywords: toxin
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-69/Product: alpha-hordothionin #status predicted <AHT>
F;70-129/Product: acidic peptide #status predicted <APE>
F;27-63,28-55,36-53,40-49/Disulfide bonds: #status predicted

Query Match 100.0%; Score 259; DB 1; Length 133;
Best Local Similarity 100.0%; Pred. No. 4.2e-21;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              |||||||||||||||||||||||||||||||||||||||||||||
Db         25 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 69
```

RESULT 2
S22977
beta-hordothionin precursor - barley

C;Species: Hordeum vulgare (barley)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 16-Jul-1999
C;Accession: S22977; A24866
R;Rasmussen, S.K.; Rasmussen, C.
submitted to the EMBL Data Library, June 1992
A;Description: Full-length cDNA clone encoding barley toxin beta-hordothionin.
A;Reference number: S22977
A;Accession: S22977
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-136 <RAS>
A;Cross-references: EMBL:Z13008; NID:g22736; PIDN:CAA78352.1; PID:g22737
R;Hernandez-Lucas, C.; Royo, J.; Paz-Ares, J.; Ponz, F.; Garcia-Olmedo, F.; Carbonero, P
FEBS Lett. 200, 103-106, 1986
A;Title: Polyadenylation site heterogeneity in mRNA encoding the precursor of the barley
A;Reference number: A24866
A;Accession: A24866
A;Molecule type: mRNA
A;Residues: 10-136 <HER>
A;Cross-references: GB:X05901
C;Superfamily: viscotoxin
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-127/Product: beta-hordothionin #status predicted <MAT>

Query Match 86.9%; Score 225; DB 2; Length 136;
Best Local Similarity 86.7%; Pred. No. 2e-17;
Matches 39; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
Db 28 KSCCRSTLGRNCYNLCRVRGAQKLCANACRCKLTSGLKCPSSFPK 72

RESULT 3
VSWTA2
alpha-2-thionin - wheat (fragment)
N;Alternate names: alpha-1-purothionin; purothionin A-II
C;Species: Triticum aestivum (common wheat)
C;Date: 24-Apr-1984 #sequence_revision 16-Feb-1996 #text_change 04-Oct-1996
C;Accession: S31670; B91945; B90018; A90913; A01807
R;Garcia-Olmedo, F.
submitted to the EMBL Data Library, January 1993
A;Reference number: S31670
A;Accession: S31670
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-125 <GAR>
A;Cross-references: EMBL:X70666
R;Ohtani, S.; Okada, T.; Yoshizumi, H.; Kagamiyama, H.
J. Biochem. 82, 753-767, 1977
A;Title: Complete primary structures of two subunits of purothionin A, a lethal protein
A;Reference number: A91945; MUID:78026451; PMID:914810
A;Accession: B91945
A;Molecule type: protein
A;Residues: 16-61 <OH1>
A;Experimental source: strain Manitoba 3
R;Ohtani, S.; Okada, T.; Kagamiyama, H.; Yoshizumi, H.
Agric. Biol. Chem. 39, 2269-2270, 1975
A;Title: The amino acid sequence of purothionin A, a lethal toxic protein from brewer's
A;Reference number: A90018
A;Accession: B90018
A;Molecule type: protein
A;Residues: 16-61 <OH2>
R;Jones, B.L.; Mak, A.S.
Cereal Chem. 54, 511-523, 1977
A;Title: Amino acid sequences of the two alpha-purothionins of hexaploid wheat.
A;Reference number: A90913
A;Accession: A90913
A;Molecule type: protein
A;Residues: 16-61 <JON>
A;Experimental source: cv. Manitou
C;Superfamily: viscotoxin
C;Keywords: seed; toxin
F;18-54,19-46,31-40,27-44/Disulfide bonds: #status predicted

Query Match 86.5%; Score 224; DB 1; Length 125;
Best Local Similarity 84.4%; Pred. No. 2.4e-17;
Matches 38; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
Db 16 KSCCRSTLGRNCYNLCRARGAQKLCAGVCRCKISSGLSCPKGFPK 60

RESULT 4
VSWTA1
purothionin A-I - wheat
N;Alternate names: beta-purothionin
C;Species: Triticum aestivum (common wheat)
C;Date: 22-Jun-1981 #sequence_revision 22-Jun-1981 #text_change 04-Oct-1996
C;Accession: A91945; A90018; A90742; A01806
R;Ohtani, S.; Okada, T.; Yoshizumi, H.; Kagamiyama, H.
J. Biochem. 82, 753-767, 1977
A;Title: Complete primary structures of two subunits of purothionin A, a lethal protein
A;Reference number: A91945; MUID:78026451; PMID:914810
A;Accession: A91945
A;Molecule type: protein
A;Residues: 1-45 <OH1>
A;Experimental source: strain Manitoba 3
R;Ohtani, S.; Okada, T.; Kagamiyama, H.; Yoshizumi, H.
Agric. Biol. Chem. 39, 2269-2270, 1975
A;Title: The amino acid sequence of purothionin A, a lethal toxic protein from brewer's
A;Reference number: A90018
A;Accession: A90018
A;Molecule type: protein
A;Residues: 1-45 <OH2>
R;Mak, A.S.; Jones, B.L.
Can. J. Biochem. 22, 835-842, 1976
A;Title: The amino acid sequence of wheat beta-purothionin.
A;Reference number: A90742
A;Accession: A90742
A;Molecule type: protein
A;Residues: 1-45 <MAK>
A;Note: this protein is called beta-purothionin by the authors
C;Superfamily: viscotoxin
C;Keywords: seed; toxin
F;3-39,4-31,12-29,16-25/Disulfide bonds: #status predicted

Query Match 82.6%; Score 214; DB 1; Length 45;
Best Local Similarity 82.2%; Pred. No. 1.4e-16;
Matches 37; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
Db 1 KSCCKSTLGRNCYNLCRARGAQKLCANVCRCKLTSGLSCPKDFPK 45

RESULT 5
S31695
alpha-1-thionin - wheat
C;Species: Triticum aestivum (common wheat)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 16-Jul-1999
C;Accession: S31695
R;Garcia-Olmedo, F.
submitted to the EMBL Data Library, January 1993
A;Reference number: S31670
A;Accession: S31695
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-136 <GAR>
A;Cross-references: EMBL:X70665; NID:g21845; PIDN:CAA50003.1; PID:g21846
C;Superfamily: viscotoxin

Query Match 82.6%; Score 214; DB 2; Length 136;
Best Local Similarity 82.2%; Pred. No. 3e-16;
Matches 37; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

```
Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              |||||:|||||||||||| |||||||: ||||||||   || ||||
Db         28 KSCCRTTLGRNCYNLCRSRGAQKLCSTVCRCKLTSGLSCPKGFPK 72


RESULT 6
S07648
thionin precursor, leaf - barley
N;Alternate names: thionin BTH6
C;Species: Hordeum vulgare (barley)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 25-Oct-1996
C;Accession: S07648; S06349; S00825; A38776
R;Apel, K.
submitted to the EMBL Data Library, April 1988
A;Reference number: S07648
A;Accession: S07648
A;Molecule type: mRNA
A;Residues: 1-137 <APE>
R;Bohlmann, H.; Apel, K.
Mol. Gen. Genet. 207, 446-454, 1987
A;Title: Isolation and characterization of cDNAs coding for leaf-specific thionins close
A;Reference number: S06349
A;Accession: S06349
A;Molecule type: mRNA
A;Residues: 1-33,'A',35-137 <BOH>
A;Cross-references: EMBL:X05576
A;Experimental source: clone DB4
A;Note: this sequence has been revised in reference S07648
R;Bohlmann, H.; Clausen, S.; Behnke, S.; Giese, H.; Hiller, C.; Reimann-Philipp, U.; Sch
EMBO J. 7, 1559-1565, 1988
A;Title: Leaf-specific thionins of barley - a novel class of cell wall proteins toxic to
A;Reference number: S00825
A;Accession: S00825
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 29-44,'R',46-74 <BO2>
A;Accession: A38776
A;Molecule type: protein
A;Residues: 'XXXX',33-39,'X',41-43,'XX',46-50,'K',52-53,'X',55-57,'XXX',61-63 <BO3>
A;Note: 34-Gln, 35-Val, 39-Leu, 41-Pro, 43-Ile, 56-Ala, and 61-Val were also found
C;Comment: This protein is toxic against plant-pathogenic fungi.
C;Genetics:
A;Map position: 6
C;Superfamily: viscotoxin
C;Keywords: antifungal; cell wall; toxin
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-74/Product: thionin #status predicted <MAT>

  Query Match             62.4%;  Score 161.5;  DB 2;  Length 137;
  Best Local Similarity   56.5%;  Pred. No. 1.3e-10;
  Matches   26;  Conservative    6;  Mismatches   13;  Indels    1;  Gaps    1;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQK-LCAGVCRCKLTSSGKCPTGFPK 45
              ||||: || ||||| |   |  : :||| ||||: |  |||: :||
Db         29 KSCCKDTLARNCYNTCHFAGGSRPVCAGACRCKIISGPKCPSDYPK 74


RESULT 7
A24074
pyrularia thionin - oil nut
C;Species: Pyrularia pubera (oil nut, buffalo nut)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A24074
R;Vernon, L.P.; Evett, G.E.; Zeikus, R.D.; Gray, W.R.
Arch. Biochem. Biophys. 238, 18-29, 1985
A;Title: A toxic thionin from Pyrularia pubera: purification, properties, and amino acid
A;Reference number: A24074; MUID:85173323; PMID:3985614
A;Accession: A24074
A;Molecule type: protein
A;Residues: 1-47 <VER>
C;Superfamily: viscotoxin

  Query Match             56.4%;  Score 146;  DB 1;  Length 47;
  Best Local Similarity   51.1%;  Pred. No. 2.9e-09;
  Matches   24;  Conservative   10;  Mismatches   11;  Indels    2;  Gaps    1;

Qy          1 KSCCRSTLGRNCYNLCRVRG--AQKLCAGVCRCKLTSSGKCPTGFPK 45
              |||||:|  |||||:||: |  ::::||  | ||: |   ||: :||
Db          1 KSCCRNTWARNCYNVCRLPGTISREICAKKCDCKIISGTTCPSDYPK 47


RESULT 8
S22515
thionin precursor, leaf - barley
N;Alternate names: jasmonate-induced protein 2
C;Species: Hordeum vulgare (barley)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
C;Accession: S22515
R;Andresen, I.; Becker, W.; Schlueter, K.; Burges, J.; Parthier, B.; Apel, K.
Plant Mol. Biol. 19, 193-204, 1992
A;Title: The identification of leaf thionin as one of the main jasmonate-induced protein
A;Reference number: S22514; MUID:92322947; PMID:1377959
A;Accession: S22515
A;Molecule type: mRNA
A;Residues: 1-137 <AND>
A;Cross-references: EMBL:S39760
C;Superfamily: viscotoxin

  Query Match             56.2%;  Score 145.5;  DB 2;  Length 137;
  Best Local Similarity   52.2%;  Pred. No. 7.1e-09;
  Matches   24;  Conservative    6;  Mismatches   15;  Indels    1;  Gaps    1;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQK-LCAGVCRCKLTSSGKCPTGFPK 45
              ||||::| |||||| ||  |  : :||  | ||: |   ||  :||
Db         29 KSCCKNTTGRNCYNACRFAGGSRPVCATACGCKIISGPTCPRDYPK 74


RESULT 9
S16099
viscotoxin - European mistletoe
C;Species: Viscum album (European mistletoe)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C;Accession: S16099
R;Schrader, G.; Apel, K.
Eur. J. Biochem. 198, 549-553, 1991
A;Title: Isolation and characterization of cDNAs encoding viscotoxins of mistletoe (Visc
A;Reference number: S16099; MUID:91266934; PMID:1710983
A;Accession: S16099
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-111 <EUR>
C;Superfamily: viscotoxin

  Query Match             50.0%;  Score 129.5;  DB 2;  Length 111;
  Best Local Similarity   50.0%;  Pred. No. 3.2e-07;
  Matches   23;  Conservative    7;  Mismatches   15;  Indels    1;  Gaps    1;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQK-LCAGVCRCKLTSSGKCPTGFPK 45
              |||| :| ||| || ||: || :  || :  ||: |   ||: :||
Db         27 KSCCPNTTGRNIYNACRLTGAPRPTCAKLSGCKIISGSTCPSDYPK 72


RESULT 10
S52554
thionin variant Thi2Ca11 - Abyssinian crambe
C;Species: Crambe abyssinica (Abyssinian crambe)
C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 16-Feb-1997
C;Accession: S52554
R;Schrader-Fischer, G.; Apel, K.
Mol. Gen. Genet. 245, 380-389, 1994
A;Title: Organ-specific expression of highly divergent thionin variants that are distinc
A;Reference number: S52545; MUID:95115690; PMID:7816048
A;Accession: S52554
A;Status: preliminary
A;Molecule type: mRNA
```

```
A;Residues: 1-133 <SCH>
C;Superfamily: viscotoxin

  Query Match             45.8%;  Score 118.5;  DB 2;  Length 133;
  Best Local Similarity   46.7%;  Pred. No. 5.6e-06;
  Matches   21;  Conservative    7;  Mismatches   16;  Indels    1;  Gaps    1;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQK-LCAGVCRCKLTSSGKCPTGFP 44
              |||| |    || ||:||: |  : :|| :  ||: |  |||:  |
Db         24 KSCCPSITARNTYNVCRLPGTPRPVCASISGCKILSVTKCPSNLP 68


RESULT 11
VTVAA2
viscotoxin A2 - European mistletoe
C;Species: Viscum album (European mistletoe)
C;Date: 13-Jul-1981 #sequence_revision 08-Oct-1981 #text_change 04-Oct-1996
C;Accession: A90005; A01799
R;Olson, T.; Samuelsson, G.
Acta Chem. Scand. 26, 585-595, 1972
A;Title: The amino acid sequence of viscotoxin A2 from the European mistletoe (Viscum al
A;Reference number: A90005; MUID:72211843; PMID:5035954
A;Accession: A90005
A;Molecule type: protein
A;Residues: 1-46 <OLS>
R;Olson, T.; Samuelsson, G.
Acta Pharm. Suec. 11, 381-386, 1974
A;Title: The disulphide bonds of viscotoxin A2 from the European mistletoe (Viscum album
A;Reference number: A90013; MUID:75015879; PMID:4607177
A;Contents: annotation; disulfide bonds
C;Superfamily: viscotoxin
C;Keywords: toxin
F;3-40,4-32/Disulfide bonds: #status predicted
F;16-26/Disulfide bonds: #status experimental

  Query Match             44.6%;  Score 115.5;  DB 1;  Length 46;
  Best Local Similarity   47.6%;  Pred. No. 5.5e-06;
  Matches   20;  Conservative    9;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          1 KSCCRSTLGRNCYNLCRV-RGAQKLCAGVCRCKLTSSGKCPT 41
              |||| :| ||| || ||   |:::|| :  ||: |:  ||:
Db          1 KSCCPNTTGRNIYNTCRFGGGSREVCASLSGCKIISASTCPS 42


RESULT 12
VTVAA3
viscotoxin A3 - European mistletoe
C;Species: Viscum album (European mistletoe)
C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 04-Oct-1996
C;Accession: A01801
R;Samuelsson, G.; Seger, L.; Olson, T.
Acta Chem. Scand. 22, 2624-2642, 1968
A;Title: The amino acid sequence of oxidized viscotoxin A3 from the European mistletoe (
A;Reference number: A90003; MUID:69157811; PMID:5719166
A;Accession: A01801
A;Molecule type: protein
A;Residues: 1-46 <SAM>
R;Samuelsson, G.; Pettersson, B.
Acta Chem. Scand. 25, 2048-2054, 1971
A;Title: The disulfide bonds of viscotoxin A3 from the European mistletoe (Viscum album
A;Reference number: A90004; MUID:72049894; PMID:4941626
A;Contents: annotation; disulfide bonds
C;Superfamily: viscotoxin
C;Keywords: toxin
F;3-40,4-32/Disulfide bonds: #status predicted
F;16-26/Disulfide bonds: #status experimental

  Query Match             44.6%;  Score 115.5;  DB 1;  Length 46;
  Best Local Similarity   50.0%;  Pred. No. 5.5e-06;
  Matches   21;  Conservative    6;  Mismatches   14;  Indels    1;  Gaps    1;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQK-LCAGVCRCKLTSSGKCPT 41
              |||| :| ||| || ||: || :  || :  ||: |   ||:
Db          1 KSCCPNTTGRNIYNACRLTGAPRPTCAKLSGCKIISGSTCPS 42


RESULT 13
VTVAB
viscotoxin B - European mistletoe
C;Species: Viscum album (European mistletoe)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 04-Oct-1996
C;Accession: A91187; A01799
R;Samuelsson, G.; Pettersson, B.M.
Eur. J. Biochem. 21, 86-89, 1971
A;Title: The amino acid sequence of viscotoxin B from the European mistletoe (Viscum al
A;Reference number: A91187; MUID:71284202; PMID:5568678
A;Accession: A91187
A;Molecule type: protein
A;Residues: 1-46 <SAM>
C;Superfamily: viscotoxin
C;Keywords: toxin
F;3-40,4-32,16-26/Disulfide bonds: #status predicted

  Query Match             44.2%;  Score 114.5;  DB 1;  Length 46;
  Best Local Similarity   47.6%;  Pred. No. 7.1e-06;
  Matches   20;  Conservative    9;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          1 KSCCRSTLGRNCYNLCRV-RGAQKLCAGVCRCKLTSSGKCPT 41
              |||| :| ||| || ||:  |::: || :  ||: |:  ||:
Db          1 KSCCPNTTGRNIYNTCRLGGGSRERCASLSGCKIISASTCPS 42


RESULT 14
DKDCB
denclatoxin B - Columbia mistletoe
C;Species: Dendrophthora clavata (Columbia mistletoe)
C;Date: 30-Apr-1981 #sequence_revision 30-Apr-1981 #text_change 04-Oct-1996
C;Accession: A01804
R;Samuelsson, G.; Pettersson, B.
Acta Pharm. Suec. 14, 245-254, 1977
A;Title: Toxic proteins from the mistletoe Dendrophthora clavata.
A;Reference number: A01804; MUID:78016835; PMID:906843
A;Accession: A01804
A;Molecule type: protein
A;Residues: 1-46 <SAM>
C;Superfamily: viscotoxin
C;Keywords: toxin
F;3-40,4-32,16-26/Disulfide bonds: #status predicted

  Query Match             43.8%;  Score 113.5;  DB 1;  Length 46;
  Best Local Similarity   45.5%;  Pred. No. 9.1e-06;
  Matches   20;  Conservative    8;  Mismatches   15;  Indels    1;  Gaps    1;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQK-LCAGVCRCKLTSSGKCPTGF 43
              |||| :|  || ||:||: |  : :|| :  ||: |    || |:
Db          1 KSCCPTTAARNQYNICRLPGTPRPVCAALSGCKIISGTGCPPGY 44


RESULT 15
LOFDAL
ligatoxin A - Argentine mistletoe (tentative sequence)
C;Species: Phoradendron liga (Argentine mistletoe)
C;Date: 30-Apr-1981 #sequence_revision 30-Apr-1981 #text_change 31-Mar-2000
C;Accession: A01803
R;Thunberg, E.; Samuelsson, G.
Acta Pharm. Suec. 14(Suppl.), 64, 1977
A;Title: Isolation and properties of ligatoxin A, a toxic protein from the mistletoe Ph
A;Reference number: A01803
A;Accession: A01803
A;Molecule type: protein
A;Residues: 1-46 <THU>
C;Superfamily: viscotoxin
C;Keywords: toxin
F;3-40,4-32,16-26/Disulfide bonds: #status predicted

  Query Match             42.3%;  Score 109.5;  DB 1;  Length 46;
```

Best Local Similarity 45.5%; Pred. No. 2.4e-05;
Matches 20; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

```
Qy          1 KSCCRSTLGRNCYNLCRVRGAQK-LCAGVCRCKLTSSGKCPTGF 43
              |||| ||  || || ||: |  :  || :  ||: |   | :|:
Db          1 KSCCPSTTARNIYNTCRLTGTSRPTCASLSGCKIISGSTCBSGW 44
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Search completed: January 21, 2004, 09:48:36
Job time : 21 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 21, 2004, 09:46:22 ; Search time 33 Seconds
(without alignments)
278.838 Million cell updates/sec

Title: US-10-010-709-1
Perfect score: 259
Sequence: 1 KSCCRSTLGRNCYNLCRVRG.....AGVCRCKLTSSGKCPTGFPK 45

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 762491 seqs, 204481190 residues

Total number of hits satisfying chosen parameters: 762491

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	259	100.0	54	12	US-09-864-169-8	Sequence 8, Appli
2	259	100.0	88	12	US-09-864-169-11	Sequence 11, Appl
3	259	100.0	124	12	US-09-864-169-2	Sequence 2, Appli
4	259	100.0	543	12	US-09-864-169-5	Sequence 5, Appli
5	166.5	64.3	46	9	US-09-030-619-230	Sequence 230, App
6	166.5	64.3	46	12	US-10-277-233-230	Sequence 230, App
7	78	30.1	3401	15	US-10-184-644-411	Sequence 411, App
8	78	30.1	3401	15	US-10-184-634-411	Sequence 411, App
9	75.5	29.2	3781	15	US-10-184-644-453	Sequence 453, App
10	75.5	29.2	3781	15	US-10-184-634-453	Sequence 453, App
11	75	29.0	2768	12	US-10-063-685-15	Sequence 15, Appl
12	73.5	28.4	1320	12	US-10-063-685-155	Sequence 155, App
13	73.5	28.4	4842	15	US-10-184-644-289	Sequence 289, App
14	73.5	28.4	4842	15	US-10-184-634-289	Sequence 289, App
15	73	28.2	1021	15	US-10-184-644-373	Sequence 373, App
16	73	28.2	1021	15	US-10-184-634-373	Sequence 373, App
17	73	28.2	1200	9	US-09-826-508-3	Sequence 3, Appli
18	71.5	27.6	2148	15	US-10-184-644-507	Sequence 507, App
19	71.5	27.6	2148	15	US-10-184-634-507	Sequence 507, App
20	71	27.4	1664	12	US-10-140-472-169	Sequence 169, App
21	71	27.4	1664	12	US-10-141-761-169	Sequence 169, App
22	71	27.4	1664	12	US-10-142-885-169	Sequence 169, App
23	71	27.4	1664	12	US-10-158-790-169	Sequence 169, App
24	71	27.4	1664	12	US-10-137-871-169	Sequence 169, App
25	71	27.4	1664	12	US-10-140-805-169	Sequence 169, App
26	71	27.4	1664	12	US-10-140-864-169	Sequence 169, App
27	71	27.4	1664	12	US-10-140-923-169	Sequence 169, App
28	71	27.4	1664	12	US-10-141-756-169	Sequence 169, App
29	71	27.4	1664	12	US-10-141-759-169	Sequence 169, App
30	71	27.4	1664	15	US-10-123-155-169	Sequence 169, App
31	71	27.4	1664	16	US-10-146-731-169	Sequence 169, App
32	70.5	27.2	1765	15	US-10-037-182-8	Sequence 8, Appli
33	70.5	27.2	1786	9	US-09-873-676-113	Sequence 113, App
34	70.5	27.2	1786	10	US-09-938-275-6	Sequence 6, Appli
35	70.5	27.2	1786	15	US-10-037-182-6	Sequence 6, Appli
36	70	27.0	1759	15	US-10-184-644-151	Sequence 151, App
37	70	27.0	1759	15	US-10-184-634-151	Sequence 151, App
38	70	27.0	3884	12	US-10-140-472-145	Sequence 145, App
39	70	27.0	3884	12	US-10-141-761-145	Sequence 145, App
40	70	27.0	3884	12	US-10-142-885-145	Sequence 145, App
41	70	27.0	3884	12	US-10-158-790-145	Sequence 145, App
42	70	27.0	3884	12	US-10-137-871-145	Sequence 145, App
43	70	27.0	3884	12	US-10-140-805-145	Sequence 145, App
44	70	27.0	3884	12	US-10-140-864-145	Sequence 145, App
45	70	27.0	3884	12	US-10-140-923-145	Sequence 145, App

ALIGNMENTS

RESULT 1
US-09-864-169-8
; Sequence 8, Application US/09864169
; Publication No. US20030228654A1
; GENERAL INFORMATION:
; APPLICANT: IMAEDA, TAKAO
; APPLICANT: YAMADA, YUKIO
; APPLICANT: HIRAI, MASANA
; APPLICANT: SHIMAMURA, TAKASHI
; APPLICANT: KOHDA, KATSUNORI
; APPLICANT: MURAMOTO, NOBUHIKO
; TITLE OF INVENTION: METHOD FOR PRODUCING ANTIMICROBIAL PROTEIN AND FUSION PROTEIN
; FILE REFERENCE: 208377US0
; CURRENT APPLICATION NUMBER: US/09/864,169
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: JP2000-161090
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Hordeum vulgare
US-09-864-169-8

Query Match 100.0%; Score 259; DB 12; Length 54;
Best Local Similarity 100.0%; Pred. No. 4.5e-22;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              |||||||||||||||||||||||||||||||||||||||||||||
Db         10 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 54
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RESULT 2
US-09-864-169-11
; Sequence 11, Application US/09864169
; Publication No. US20030228654A1

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; GENERAL INFORMATION:
;  APPLICANT: IMAEDA, TAKAO
;  APPLICANT:  YAMADA, YUKIO
;  APPLICANT:  HIRAI, MASANA
;  APPLICANT:  SHIMAMURA, TAKASHI
;  APPLICANT:  KOHDA, KATSUNORI
;  APPLICANT:  MURAMOTO, NOBUHIKO
;  TITLE OF INVENTION: METHOD FOR PRODUCING ANTIMICROBIAL PROTEIN AND FUSION PROTEIN
;  FILE REFERENCE: 208377US0
;  CURRENT APPLICATION NUMBER: US/09/864,169
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: JP2000-161090
;  PRIOR FILING DATE: 2000-05-26
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
;   LENGTH: 88
;   TYPE: PRT
;   ORGANISM: Hordeum vulgare
US-09-864-169-11

  Query Match             100.0%;  Score 259;  DB 12;  Length 88;
  Best Local Similarity   100.0%;  Pred. No. 7.1e-22;
  Matches   45;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              |||||||||||||||||||||||||||||||||||||||||||||
Db          9 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 53


RESULT 3
US-09-864-169-2
; Sequence 2, Application US/09864169
; Publication No. US20030228654A1
; GENERAL INFORMATION:
;  APPLICANT: IMAEDA, TAKAO
;  APPLICANT:  YAMADA, YUKIO
;  APPLICANT:  HIRAI, MASANA
;  APPLICANT:  SHIMAMURA, TAKASHI
;  APPLICANT:  KOHDA, KATSUNORI
;  APPLICANT:  MURAMOTO, NOBUHIKO
;  TITLE OF INVENTION: METHOD FOR PRODUCING ANTIMICROBIAL PROTEIN AND FUSION PROTEIN
;  FILE REFERENCE: 208377US0
;  CURRENT APPLICATION NUMBER: US/09/864,169
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: JP2000-161090
;  PRIOR FILING DATE: 2000-05-26
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 124
;   TYPE: PRT
;   ORGANISM: Hordeum vulgare
US-09-864-169-2

  Query Match             100.0%;  Score 259;  DB 12;  Length 124;
  Best Local Similarity   100.0%;  Pred. No. 9.7e-22;
  Matches   45;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              |||||||||||||||||||||||||||||||||||||||||||||
Db         10 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 54


RESULT 4
US-09-864-169-5
; Sequence 5, Application US/09864169
; Publication No. US20030228654A1
; GENERAL INFORMATION:
;  APPLICANT: IMAEDA, TAKAO
;  APPLICANT:  YAMADA, YUKIO
;  APPLICANT:  HIRAI, MASANA
;  APPLICANT:  SHIMAMURA, TAKASHI
;  APPLICANT:  KOHDA, KATSUNORI
;  APPLICANT:  MURAMOTO, NOBUHIKO
;  TITLE OF INVENTION: METHOD FOR PRODUCING ANTIMICROBIAL PROTEIN AND FUSION PROTEIN
;  FILE REFERENCE: 208377US0
;  CURRENT APPLICATION NUMBER: US/09/864,169
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: JP2000-161090
;  PRIOR FILING DATE: 2000-05-26
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
;   LENGTH: 543
;   TYPE: PRT
;   ORGANISM: Hordeum vulgare
US-09-864-169-5

  Query Match             100.0%;  Score 259;  DB 12;  Length 543;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-21;
  Matches   45;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              |||||||||||||||||||||||||||||||||||||||||||||
Db          9 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 53


RESULT 5
US-09-030-619-230
; Sequence 230, Application US/09030619B
; Patent No. US20020035061A1
; GENERAL INFORMATION:
;  APPLICANT:  Krieger, Timothy J.
;  APPLICANT:  Taylor, Robert
;  APPLICANT:  Erfle, Douglas
;  APPLICANT:  Fraser, Janet R.
;  APPLICANT:  West, Michael H.P.
;  APPLICANT:  McNicol, Patricia J.
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR TREATING
;  TITLE OF INVENTION:  INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
;  TITLE OF INVENTION:  WITH ANTIBIOTICS
;  FILE REFERENCE:  660081.406
;  CURRENT APPLICATION NUMBER: US/09/030,619B
;  CURRENT FILING DATE:  1998-02-25
;  NUMBER OF SEQ ID NOS:  232
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 230
;   LENGTH: 46
;   TYPE: PRT
;   ORGANISM: Hordeum vulgare
US-09-030-619-230

  Query Match             64.3%;  Score 166.5;  DB 9;  Length 46;
  Best Local Similarity   58.7%;  Pred. No. 8.6e-12;
  Matches   27;  Conservative    6;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQK-LCAGVCRCKLTSSGKCPTGFPK 45
              ||||: || ||||| ||  |  : :||| ||||: |  |||: :||
Db          1 KSCCKDTLARNCYNTCRFAGGSRPVCAGACRCKIISGPKCPSDYPK 46


RESULT 6
US-10-277-233-230
; Sequence 230, Application US/10277233
; Publication No. US20030232750A1
; GENERAL INFORMATION:
;  APPLICANT: Krieger, Timothy J.
;  APPLICANT:  Taylor, Robert
;  APPLICANT:  Erfle, Douglas
;  APPLICANT:  Fraser, Janet R.
;  APPLICANT:  West, Michael H.P.
;  APPLICANT:  McNicol, Patricia J.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
;  TITLE OF INVENTION:  INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
;  TITLE OF INVENTION:  WITH ANTIBIOTICS
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;  FILE REFERENCE: 660081.406C1
;  CURRENT APPLICATION NUMBER: US/10/277,233
;  CURRENT FILING DATE:  2002-10-18
;  NUMBER OF SEQ ID NOS: 232
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 230
;   LENGTH: 46
;   TYPE: PRT
;   ORGANISM: Hordeum vulgare
US-10-277-233-230

  Query Match             64.3%;  Score 166.5;  DB 12;  Length 46;
  Best Local Similarity   58.7%;  Pred. No. 8.6e-12;
  Matches   27;  Conservative    6;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQK-LCAGVCRCKLTSSGKCPTGFPK 45
              ||||: || ||||| ||  |  : :||| ||||: |  |||: :||
Db          1 KSCCKDTLARNCYNTCRFAGGSRPVCAGACRCKIISGPKCPSDYPK 46


RESULT 7
US-10-184-644-411
; Sequence 411, Application US/10184644
; Publication No. US20030044930A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C227
;  CURRENT APPLICATION NUMBER: US/10/184,644
;  CURRENT FILING DATE:  2002-06-28
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 411
;   LENGTH: 3401
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-184-644-411

  Query Match             30.1%;  Score 78;  DB 15;  Length 3401;
  Best Local Similarity   35.0%;  Pred. No. 3.6;
  Matches   14;  Conservative    1;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          3 CCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTG 42
              ||    |  |    |    |  ||| | |    :| |  |
Db       2969 CCACCTGGTCCTTCATGAAGAGCAGACACTTAGAGGCTGG 3008


RESULT 8
US-10-184-634-411
; Sequence 411, Application US/10184634
; Publication No. US20030068684A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C217
;  CURRENT APPLICATION NUMBER: US/10/184,634
;  CURRENT FILING DATE:  2002-06-28
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 411
;   LENGTH: 3401
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-184-634-411

  Query Match             30.1%;  Score 78;  DB 15;  Length 3401;
  Best Local Similarity   35.0%;  Pred. No. 3.6;
  Matches   14;  Conservative    1;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          3 CCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTG 42
              ||    |  |    |    |  ||| | |    :| |  |
Db       2969 CCACCTGGTCCTTCATGAAGAGCAGACACTTAGAGGCTGG 3008


RESULT 9
US-10-184-644-453
; Sequence 453, Application US/10184644
; Publication No. US20030044930A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C227
;  CURRENT APPLICATION NUMBER: US/10/184,644
;  CURRENT FILING DATE:  2002-06-28
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 453
;   LENGTH: 3781
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-184-644-453

  Query Match             29.2%;  Score 75.5;  DB 15;  Length 3781;
  Best Local Similarity   40.5%;  Pred. No. 7.5;
  Matches   15;  Conservative    1;  Mismatches   20;  Indels    1;  Gaps    1;

Qy          3 CCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKC 39
              ||  | |  |   |   |   ||| | |  | :| |
Db       2581 CCGCTCGATC-ACCGAGGGTACCAGTCCCTGTCAGAC 2616


RESULT 10
US-10-184-634-453
; Sequence 453, Application US/10184634
; Publication No. US20030068684A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
```

```
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C217
;  CURRENT APPLICATION NUMBER: US/10/184,634
;  CURRENT FILING DATE:  2002-06-28
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 453
;   LENGTH: 3781
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-184-634-453

  Query Match            29.2%;  Score 75.5;  DB 15;  Length 3781;
  Best Local Similarity  40.5%;  Pred. No. 7.5;
  Matches   15;  Conservative    1;  Mismatches   20;  Indels    1;  Gaps    1;

Qy          3 CCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKC 39
              ||  | |  |   |  |    ||| | |  | :| |
Db       2581 CCGCTCGATC-ACCGAGGGTACCAGTCCCTGTCAGAC 2616


RESULT 11
US-10-063-685-15
; Sequence 15, Application US/10063685
; Publication No. US20030180909A1
; GENERAL INFORMATION:
;  APPLICANT: Eaton,Dan L.
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,Christopher J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3230R1C1
;  CURRENT APPLICATION NUMBER: US/10/063,685
;  CURRENT FILING DATE:  2002-05-08
;      Prior Application removed - See Palm or File Wrapper
;  NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 15
;   LENGTH: 2768
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-063-685-15

  Query Match            29.0%;  Score 75;  DB 12;  Length 2768;
  Best Local Similarity  35.9%;  Pred. No. 6.4;
  Matches   14;  Conservative    2;  Mismatches   23;  Indels    0;  Gaps    0;

Qy          3 CCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPT 41
              || :|    |   |   |    ||| | |    :| | |
Db        191 CCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTT 229


RESULT 12
US-10-063-685-155
; Sequence 155, Application US/10063685
; Publication No. US20030180909A1
; GENERAL INFORMATION:
;  APPLICANT: Eaton,Dan L.
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,Christopher J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3230R1C1
;  CURRENT APPLICATION NUMBER: US/10/063,685
;  CURRENT FILING DATE:  2002-05-08
;      Prior Application removed - See Palm or File Wrapper
;  NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 155
;   LENGTH: 1320
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-063-685-155

  Query Match            28.4%;  Score 73.5;  DB 12;  Length 1320;
  Best Local Similarity  35.7%;  Pred. No. 4.8;
  Matches   15;  Conservative    2;  Mismatches   24;  Indels    1;  Gaps    1;

Qy          2 SCCRSTLGRNCYNLCRVRG-AQKLCAGVCRCKLTSSGKCPTG 42
              :||  | |  |   |  |  |      | | | |    :| | ||
Db        438 TCCCCTAGAGCCTGCTAGGCCCAACCGCCACCCAGAGTCCTG 479


RESULT 13
US-10-184-644-289
; Sequence 289, Application US/10184644
; Publication No. US20030044930A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C227
;  CURRENT APPLICATION NUMBER: US/10/184,644
;  CURRENT FILING DATE:  2002-06-28
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 289
;   LENGTH: 4842
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-184-644-289

  Query Match            28.4%;  Score 73.5;  DB 15;  Length 4842;
  Best Local Similarity  33.3%;  Pred. No. 16;
  Matches   15;  Conservative    3;  Mismatches   22;  Indels    5;  Gaps    1;

Qy          3 CCRSTLGRNCYN-----LCRVRGAQKLCAGVCRCKLTSSGKCPTG 42
              || :  |  |          |   ||   | | | |   :| | ||
Db       2384 CCCAGAGAGCTGTCCGCCCTCCGACACCTGACGCTTATTGACCTG 2428


RESULT 14
US-10-184-634-289
; Sequence 289, Application US/10184634
; Publication No. US20030068684A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
```

```
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C217
;  CURRENT APPLICATION NUMBER: US/10/184,634
;  CURRENT FILING DATE:  2002-06-28
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 289
;   LENGTH: 4842
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-184-634-289

  Query Match             28.4%;  Score 73.5;  DB 15;  Length 4842;
  Best Local Similarity   33.3%;  Pred. No. 16;
  Matches   15;  Conservative    3;  Mismatches   22;  Indels    5;  Gaps    1;

Qy          3 CCRSTLGRNCYN-----LCRVRGAQKLCAGVCRCKLTSSGKCPTG 42
              || :  |  |          |  ||   | | |  |   ::| | ||
Db       2384 CCCAGAGAGCTGTCCGCCCTCCGACACCTGACGCTTATTGACCTG 2428


RESULT 15
US-10-184-644-373
; Sequence 373, Application US/10184644
; Publication No. US20030044930A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C227
;  CURRENT APPLICATION NUMBER: US/10/184,644
;  CURRENT FILING DATE:  2002-06-28
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 373
;   LENGTH: 1021
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-184-644-373

  Query Match             28.2%;  Score 73;  DB 15;  Length 1021;
  Best Local Similarity   33.3%;  Pred. No. 4.3;
  Matches   13;  Conservative    1;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          3 CCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPT 41
              ||  |  |  |    |    |    |  |    : | | |
Db        260 CCTGTTGGGCATTCTGGAAAACCTTCCGCTCCTGGACAT 298


Search completed: January 21, 2004, 09:49:57
Job time : 33 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 21, 2004, 09:46:02 ; Search time 22 Seconds
(without alignments)
86.545 Million cell updates/sec

Title: US-10-010-709-1
Perfect score: 259
Sequence: 1 KSCCRSTLGRNCYNLCRVRG.....AGVCRCKLTSSGKCPTGFPK 45

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	259	100.0	45	1	US-08-608-786-1	Sequence 1, Appli
2	259	100.0	45	2	US-08-824-379-1	Sequence 1, Appli
3	259	100.0	45	2	US-08-824-382-1	Sequence 1, Appli
4	259	100.0	45	2	US-08-838-763-1	Sequence 1, Appli
5	247	95.4	45	2	US-08-838-763-3	Sequence 3, Appli
6	244	94.2	45	2	US-08-838-763-2	Sequence 2, Appli
7	235	90.7	45	2	US-08-838-763-7	Sequence 7, Appli
8	231	89.2	45	1	US-08-608-786-2	Sequence 2, Appli
9	231	89.2	45	2	US-08-824-382-2	Sequence 2, Appli
10	231	89.2	45	2	US-08-838-763-8	Sequence 8, Appli
11	231	89.2	45	3	US-08-719-500-1	Sequence 1, Appli
12	225	86.9	45	2	US-08-838-763-4	Sequence 4, Appli
13	224	86.5	45	1	US-07-973-852-1	Sequence 1, Appli
14	224	86.5	45	1	US-07-950-773-1	Sequence 1, Appli
15	214	82.6	45	1	US-07-973-852-2	Sequence 2, Appli
16	214	82.6	45	1	US-07-973-852-3	Sequence 3, Appli
17	214	82.6	45	1	US-07-950-773-2	Sequence 2, Appli
18	214	82.6	45	1	US-07-950-773-3	Sequence 3, Appli
19	209	80.7	45	2	US-08-838-763-5	Sequence 5, Appli
20	202	78.0	45	2	US-08-838-763-6	Sequence 6, Appli
21	200	77.2	45	2	US-08-824-379-2	Sequence 2, Appli
22	182	70.3	45	1	US-08-608-786-3	Sequence 3, Appli
23	182	70.3	45	2	US-08-824-382-3	Sequence 3, Appli
24	170	65.6	45	2	US-08-824-379-3	Sequence 3, Appli
25	169	65.3	45	2	US-08-838-763-9	Sequence 9, Appli
26	166.5	64.3	46	4	US-09-030-619-230	Sequence 230, App
27	146	56.4	47	5	PCT-US96-08811-2	Sequence 2, Appli
28	73.5	28.4	249	4	US-09-252-991A-28972	Sequence 28972, A
29	70.5	27.2	278	2	US-08-460-309-13	Sequence 13, Appl
30	70.5	27.2	278	2	US-08-125-077-13	Sequence 13, Appl
31	70.5	27.2	279	1	US-08-152-019A-29	Sequence 29, Appl
32	70.5	27.2	1196	1	US-08-144-121-4	Sequence 4, Appli
33	70.5	27.2	1196	2	US-08-735-893-4	Sequence 4, Appli
34	69.5	26.8	271	1	US-08-152-019A-28	Sequence 28, Appl
35	63	24.3	1400	4	US-08-630-915A-37	Sequence 37, Appl
36	62.5	24.1	93	1	US-08-464-339A-13	Sequence 13, Appl
37	62.5	24.1	180	4	US-09-461-688-4	Sequence 4, Appli
38	62.5	24.1	348	1	US-08-468-847B-14	Sequence 14, Appl
39	62.5	24.1	349	1	US-08-167-628-2	Sequence 2, Appli
40	62.5	24.1	349	1	US-08-386-680-2	Sequence 2, Appli
41	62.5	24.1	349	1	US-08-459-717-2	Sequence 2, Appli
42	62.5	24.1	349	1	US-08-712-302-2	Sequence 2, Appli
43	62.5	24.1	349	2	US-08-880-031-2	Sequence 2, Appli
44	62.5	24.1	349	3	US-09-054-368-2	Sequence 2, Appli
45	62.5	24.1	349	3	US-09-097-179-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-608-786-1
; Sequence 1, Application US/08608786
; Patent No. 5703049
; GENERAL INFORMATION:
; APPLICANT: Rao, A. Gururaj
; TITLE OF INVENTION: High Methionine Derivatives of
; TITLE OF INVENTION: Alpha-Hordothionin for Pathogen-Control
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pioneer Hi-Bred International, Inc.
; STREET: 700 Capital Square, 400 Locust Street
; CITY: Des Moines
; STATE: Iowa
; COUNTRY: United States of America
; ZIP: 50309
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/608,786
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Simon, Soma G.
; REGISTRATION NUMBER: 37,444
; REFERENCE/DOCKET NUMBER: 456-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 515-248-4896
; TELEFAX: 515-248-4844
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-608-786-1

Query Match 100.0%; Score 259; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.5e-21;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              |||||||||||||||||||||||||||||||||||||||||||||
Db          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
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RESULT 2
US-08-824-379-1

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; Sequence 1, Application US/08824379
; Patent No. 5885801
;  GENERAL INFORMATION:
;    APPLICANT:  Rao, A. Gururaj
;    TITLE OF INVENTION:  High Threonine Derivatives of
;    TITLE OF INVENTION:  Alpha-Hordothionin
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pioneer Hi-Bred International, Inc.
;      STREET:  700 Capital Square, 400 Locust Street
;      CITY:  Des Moines
;      STATE:  Iowa
;      COUNTRY:  United States of America
;      ZIP:  50309
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/824,379
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/459,180
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Simon, Soma G.
;      REGISTRATION NUMBER:  37,444
;      REFERENCE/DOCKET NUMBER:  354-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  515-248-4896
;      TELEFAX:  515-248-4844
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  45 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-824-379-1

  Query Match             100.0%;  Score 259;  DB 2;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-21;
  Matches   45;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              |||||||||||||||||||||||||||||||||||||||||||||
Db          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45


RESULT 3
US-08-824-382-1
; Sequence 1, Application US/08824382
; Patent No. 5885802
;  GENERAL INFORMATION:
;    APPLICANT:  Rao, A. Gururaj
;    TITLE OF INVENTION:  High Methionine Derivatives of
;    TITLE OF INVENTION:  Alpha-Hordothionin
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pioneer Hi-Bred International, Inc.
;      STREET:  700 Capital Square, 400 Locust Street
;      CITY:  Des Moines
;      STATE:  Iowa
;      COUNTRY:  United States of America
;      ZIP:  50309
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/824,382
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/460,440
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Simon, Soma G.
;      REGISTRATION NUMBER:  37,444
;      REFERENCE/DOCKET NUMBER:  355-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  515-248-4896
;      TELEFAX:  515-248-4844
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  45 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-824-382-1

  Query Match             100.0%;  Score 259;  DB 2;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-21;
  Matches   45;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              |||||||||||||||||||||||||||||||||||||||||||||
Db          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45


RESULT 4
US-08-838-763-1
; Sequence 1, Application US/08838763
; Patent No. 5990389
;  GENERAL INFORMATION:
;    APPLICANT:  Rao, A. Gururaj
;    APPLICANT:  Beach, Larry
;    TITLE OF INVENTION:  High Lysine Derivatives of
;    TITLE OF INVENTION:  Alpha-Hordothionin
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pioneer Hi-Bred International, Inc.
;      STREET:  7100 NW 62nd Avenue, P.O. Box 1000
;      CITY:  Johnston
;      STATE:  IA
;      COUNTRY:  USA
;      ZIP:  50131
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/838,763
;      FILING DATE:  10-APR-1997
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/003,885
;      FILING DATE:  13-JAN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Michel, Marianne H
;      REGISTRATION NUMBER:  35,286
;      REFERENCE/DOCKET NUMBER:  0233C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  515-334-4467
;      TELEFAX:  515-334-6883
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  45 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-838-763-1
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  Query Match             100.0%;  Score 259;  DB 2;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-21;
  Matches   45;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              |||||||||||||||||||||||||||||||||||||||||||||
Db          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45


RESULT 5
US-08-838-763-3
; Sequence 3, Application US/08838763
; Patent No. 5990389
;  GENERAL INFORMATION:
;    APPLICANT:  Rao, A. Gururaj
;    APPLICANT:  Beach, Larry
;    TITLE OF INVENTION:  High Lysine Derivatives of
;    TITLE OF INVENTION:  Alpha-Hordothionin
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pioneer Hi-Bred International, Inc.
;      STREET:  7100 NW 62nd Avenue, P.O. Box 1000
;      CITY:  Johnston
;      STATE:  IA
;      COUNTRY:  USA
;      ZIP:  50131
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/838,763
;      FILING DATE:  10-APR-1997
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/003,885
;      FILING DATE:  13-JAN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Michel, Marianne H
;      REGISTRATION NUMBER:  35,286
;      REFERENCE/DOCKET NUMBER:  0233C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  515-334-4467
;      TELEFAX:  515-334-6883
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  45 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-838-763-3

  Query Match             95.4%;  Score 247;  DB 2;  Length 45;
  Best Local Similarity   91.1%;  Pred. No. 4.8e-20;
  Matches   41;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              ||||:|||||||||||:|:|||||||||:|||||||||||||||||
Db          1 KSCCKSTLGRNCYNLCKVKGAQKLCAGVCKCKLTSSGKCPTGFPK 45


RESULT 6
US-08-838-763-2
; Sequence 2, Application US/08838763
; Patent No. 5990389
;  GENERAL INFORMATION:
;    APPLICANT:  Rao, A. Gururaj
;    APPLICANT:  Beach, Larry
;    TITLE OF INVENTION:  High Lysine Derivatives of
;    TITLE OF INVENTION:  Alpha-Hordothionin
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pioneer Hi-Bred International, Inc.
;      STREET:  7100 NW 62nd Avenue, P.O. Box 1000
;      CITY:  Johnston
;      STATE:  IA
;      COUNTRY:  USA
;      ZIP:  50131
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/838,763
;      FILING DATE:  10-APR-1997
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/003,885
;      FILING DATE:  13-JAN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Michel, Marianne H
;      REGISTRATION NUMBER:  35,286
;      REFERENCE/DOCKET NUMBER:  0233C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  515-334-4467
;      TELEFAX:  515-334-6883
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  45 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-838-763-2

  Query Match             94.2%;  Score 244;  DB 2;  Length 45;
  Best Local Similarity   88.9%;  Pred. No. 1e-19;
  Matches   40;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              ||||:||||:||||||:|:||||||||||:|||||||||||||||||
Db          1 KSCCKSTLGKNCYNLCKVKGAQKLCAGVCKCKLTSSGKCPTGFPK 45


RESULT 7
US-08-838-763-7
; Sequence 7, Application US/08838763
; Patent No. 5990389
;  GENERAL INFORMATION:
;    APPLICANT:  Rao, A. Gururaj
;    APPLICANT:  Beach, Larry
;    TITLE OF INVENTION:  High Lysine Derivatives of
;    TITLE OF INVENTION:  Alpha-Hordothionin
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pioneer Hi-Bred International, Inc.
;      STREET:  7100 NW 62nd Avenue, P.O. Box 1000
;      CITY:  Johnston
;      STATE:  IA
;      COUNTRY:  USA
;      ZIP:  50131
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/838,763
;      FILING DATE:  10-APR-1997
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
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;      APPLICATION NUMBER:  08/003,885
;      FILING DATE:  13-JAN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Michel, Marianne H
;      REGISTRATION NUMBER:  35,286
;      REFERENCE/DOCKET NUMBER:  0233C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  515-334-4467
;      TELEFAX:  515-334-6883
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  45 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-838-763-7

  Query Match             90.7%;  Score 235;  DB 2;  Length 45;
  Best Local Similarity   86.7%;  Pred. No. 9.1e-19;
  Matches   39;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              ||||:||||| |||||:|:||||||||||:|||||||||| ||||
Db          1 KSCCKSTLGRKCYNLCKVKGAQKLCAGVCKCKLTSSGKCPKGFPK 45


RESULT 8
US-08-608-786-2
; Sequence 2, Application US/08608786
; Patent No. 5703049
;  GENERAL INFORMATION:
;    APPLICANT:  Rao, A. Gururaj
;    TITLE OF INVENTION:  High Methionine Derivatives of
;    TITLE OF INVENTION:  Alpha-Hordothionin for Pathogen-Control
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pioneer Hi-Bred International, Inc.
;      STREET:  700 Capital Square, 400 Locust Street
;      CITY:  Des Moines
;      STATE:  Iowa
;      COUNTRY:  United States of America
;      ZIP:  50309
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/608,786
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Simon, Soma G.
;      REGISTRATION NUMBER:  37,444
;      REFERENCE/DOCKET NUMBER:  456-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  515-248-4896
;      TELEFAX:  515-248-4844
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  45 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-608-786-2

  Query Match             89.2%;  Score 231;  DB 1;  Length 45;
  Best Local Similarity   84.4%;  Pred. No. 2.4e-18;
  Matches   38;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              |||||||:|| |||:||:||| ||||||||||:||||||| ||||
Db          1 KSCCRSTMGRMCYNMCRMRGAMKLCAGVCRCKMTSSGKCPMGFPK 45


RESULT 9
US-08-824-382-2
; Sequence 2, Application US/08824382
; Patent No. 5885802
;  GENERAL INFORMATION:
;    APPLICANT:  Rao, A. Gururaj
;    TITLE OF INVENTION:  High Methionine Derivatives of
;    TITLE OF INVENTION:  Alpha-Hordothionin
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pioneer Hi-Bred International, Inc.
;      STREET:  700 Capital Square, 400 Locust Street
;      CITY:  Des Moines
;      STATE:  Iowa
;      COUNTRY:  United States of America
;      ZIP:  50309
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/824,382
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/460,440
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Simon, Soma G.
;      REGISTRATION NUMBER:  37,444
;      REFERENCE/DOCKET NUMBER:  355-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  515-248-4896
;      TELEFAX:  515-248-4844
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  45 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-824-382-2

  Query Match             89.2%;  Score 231;  DB 2;  Length 45;
  Best Local Similarity   84.4%;  Pred. No. 2.4e-18;
  Matches   38;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              |||||||:|| |||:||:||| ||||||||||:||||||| ||||
Db          1 KSCCRSTMGRMCYNMCRMRGAMKLCAGVCRCKMTSSGKCPMGFPK 45


RESULT 10
US-08-838-763-8
; Sequence 8, Application US/08838763
; Patent No. 5990389
;  GENERAL INFORMATION:
;    APPLICANT:  Rao, A. Gururaj
;    APPLICANT:  Beach, Larry
;    TITLE OF INVENTION:  High Lysine Derivatives of
;    TITLE OF INVENTION:  Alpha-Hordothionin
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pioneer Hi-Bred International, Inc.
;      STREET:  7100 NW 62nd Avenue, P.O. Box 1000
;      CITY:  Johnston
;      STATE:  IA
;      COUNTRY:  USA
;      ZIP:  50131
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
```

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;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ for Windows Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/838,763
;       FILING DATE:  10-APR-1997
;       CLASSIFICATION:  800
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/003,885
;       FILING DATE:  13-JAN-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Michel, Marianne H
;       REGISTRATION NUMBER:  35,286
;       REFERENCE/DOCKET NUMBER:  0233C3
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  515-334-4467
;       TELEFAX:  515-334-6883
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  45 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-838-763-8

  Query Match             89.2%;  Score 231;  DB 2;  Length 45;
  Best Local Similarity   84.4%;  Pred. No. 2.4e-18;
  Matches   38;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              ||||:||||| |||||:|:||:|||||||:|||||||||| ||||
Db          1 KSCCKSTLGRKCYNLCKVKGAKKLCAGVCKCKLTSSGKCPKGFPK 45


RESULT 11
US-08-719-500-1
; Sequence 1, Application US/08719500
; Patent No. 6080913
;  GENERAL INFORMATION:
;    APPLICANT:  Mitchell C. Tarczynski and Rudolf Jung
;    TITLE OF INVENTION:  A BINARY METHOD OF
;    TITLE OF INVENTION:  INCREASING ACCUMULATION OF ESSENTIAL AMINO
;    TITLE OF INVENTION:  ACIDS IN SEEDS
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pioneer Hi-Bred International, Inc.
;      STREET:  7100 N.W. 62nd Avenue
;      STREET:  Post Office Box 1000
;      CITY:  Johnston
;      STATE:  Iowa
;      COUNTRY:  United States of America
;      ZIP:  50131
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch,
;      MEDIUM TYPE:  1.44 Mb storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  MS-DOS, Microsoft Windows
;      SOFTWARE:  Microsoft Windows No. 6080913epad
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/719,500
;      FILING DATE:
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SIMON, Soma G.
;      REGISTRATION NUMBER:  37,444
;      REFERENCE/DOCKET NUMBER:  0473 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (515) 248-4896
;      TELEFAX:  (515) 334-6883
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  45 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    DESCRIPTION:  hordothionin derivative
US-08-719-500-1

  Query Match             89.2%;  Score 231;  DB 3;  Length 45;
  Best Local Similarity   84.4%;  Pred. No. 2.4e-18;
  Matches   38;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              ||||:||||| |||||:|:||:|||||||:|||||||||| ||||
Db          1 KSCCKSTLGRKCYNLCKVKGAKKLCAGVCKCKLTSSGKCPKGFPK 45


RESULT 12
US-08-838-763-4
; Sequence 4, Application US/08838763
; Patent No. 5990389
;  GENERAL INFORMATION:
;    APPLICANT:  Rao, A. Gururaj
;    APPLICANT:  Beach, Larry
;    TITLE OF INVENTION:  High Lysine Derivatives of
;    TITLE OF INVENTION:  Alpha-Hordothionin
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pioneer Hi-Bred International, Inc.
;      STREET:  7100 NW 62nd Avenue, P.O. Box 1000
;      CITY:  Johnston
;      STATE:  IA
;      COUNTRY:  USA
;      ZIP:  50131
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/838,763
;      FILING DATE:  10-APR-1997
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/003,885
;      FILING DATE:  13-JAN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Michel, Marianne H
;      REGISTRATION NUMBER:  35,286
;      REFERENCE/DOCKET NUMBER:  0233C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  515-334-4467
;      TELEFAX:  515-334-6883
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  45 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-838-763-4

  Query Match             86.9%;  Score 225;  DB 2;  Length 45;
  Best Local Similarity   86.7%;  Pred. No. 1.1e-17;
  Matches   39;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              ||||:|||||| |||||:|:|||||||||:|||||||||||||||
Db          1 KSCCKSTLGRNKYNLCKVKGAQKLCAGVTKCKLTSSGKCPTGFPK 45


RESULT 13
```

```
US-07-973-852-1
; Sequence 1, Application US/07973852
; Patent No. 5376640
;  GENERAL INFORMATION:
;    APPLICANT:  Miyazaki, Toshiyuki
;    APPLICANT:  Motoi, Hirofumi
;    APPLICANT:  Kodama, Toshiaki
;    APPLICANT:  Maeda, Taturo
;    APPLICANT:  Tsujita, Takahiro
;    APPLICANT:  Okuda, Hiromichi
;    TITLE OF INVENTION:  LIPOLYTIC ENZYME INHIBITORS
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 Jefferson Davis Highway, Fourth Floor
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/973,852
;      FILING DATE:
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/631,321
;      FILING DATE:  20-DEC-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 332884/1989
;      FILING DATE:  25-DEC-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 75600/1990
;      FILING DATE:  27-MAR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 194782/1990
;      FILING DATE:  25-JUL-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Oblon, No. 5376640man F.
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  1327-014-0 DIV
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)521-4500
;      TELEFAX:  (703)486-2347
;      TELEX:  248855 OPAT UR
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  45 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-973-852-1

  Query Match             86.5%;  Score 224;  DB 1;  Length 45;
  Best Local Similarity   84.4%;  Pred. No. 1.3e-17;
  Matches   38;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              |||||||||||||||| ||||||||||||::|   || ||||
Db          1 KSCCRSTLGRNCYNLCRARGAQKLCAGVCRCKISSGLSCPKGFPK 45


RESULT 14
US-07-950-773-1
; Sequence 1, Application US/07950773
; Patent No. 5411956
;  GENERAL INFORMATION:
;    APPLICANT:  Miyazaki, Toshiyuki
;    APPLICANT:  Motoi, Hirofumi
;    APPLICANT:  Kodama, Toshiaki
;    APPLICANT:  Maeda, Taturo
;    APPLICANT:  Tsujita, Takahiro
;    APPLICANT:  Okuda, Hiromichi
;    TITLE OF INVENTION:  LIPOLYTIC ENZYME INHIBITORS
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER &
;      ADDRESSEE:  NEUSTADT, P.C.
;      STREET:  1755 Jefferson Davis Highway, Fourth Floor
;      CITY:  Arlington
;      STATE:  Virginia
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/950,773
;      FILING DATE:  19920924
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/631,321
;      FILING DATE:  20-DEC-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Oblon, No. 5411956man F.
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  1327-003-0
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)521-4500
;      TELEFAX:  (703)486-2347
;      TELEX:  248855 OPAT UR
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  45 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-950-773-1

  Query Match             86.5%;  Score 224;  DB 1;  Length 45;
  Best Local Similarity   84.4%;  Pred. No. 1.3e-17;
  Matches   38;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              |||||||||||||||| ||||||||||||::|   || ||||
Db          1 KSCCRSTLGRNCYNLCRARGAQKLCAGVCRCKISSGLSCPKGFPK 45


RESULT 15
US-07-973-852-2
; Sequence 2, Application US/07973852
; Patent No. 5376640
;  GENERAL INFORMATION:
;    APPLICANT:  Miyazaki, Toshiyuki
;    APPLICANT:  Motoi, Hirofumi
;    APPLICANT:  Kodama, Toshiaki
;    APPLICANT:  Maeda, Taturo
;    APPLICANT:  Tsujita, Takahiro
;    APPLICANT:  Okuda, Hiromichi
;    TITLE OF INVENTION:  LIPOLYTIC ENZYME INHIBITORS
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 Jefferson Davis Highway, Fourth Floor
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
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;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/973,852
;       FILING DATE:
;       CLASSIFICATION:  530
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/631,321
;       FILING DATE:  20-DEC-1990
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 332884/1989
;       FILING DATE:  25-DEC-1989
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 75600/1990
;       FILING DATE:  27-MAR-1990
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 194782/1990
;       FILING DATE:  25-JUL-1990
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Oblon, No. 5376640man F.
;       REGISTRATION NUMBER:  24,618
;       REFERENCE/DOCKET NUMBER:  1327-014-0 DIV
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (703)521-4500
;       TELEFAX:  (703)486-2347
;       TELEX:  248855 OPAT UR
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  45 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-07-973-852-2

  Query Match             82.6%;  Score 214;  DB 1;  Length 45;
  Best Local Similarity   82.2%;  Pred. No. 1.6e-16;
  Matches   37;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              |||||:|||||||||||| |||||||: ||||||||   || ||||
Db          1 KSCCRTTLGRNCYNLCRSRGAQKLCSTVCRCKLTSGLSCPKGFPK 45


Search completed: January 21, 2004, 09:49:11
Job time : 22 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 21, 2004, 09:44:07 ; Search time 41 Seconds
(without alignments)
174.212 Million cell updates/sec

Title: US-10-010-709-1
Perfect score: 259
Sequence: 1 KSCCRSTLGRNCYNLCRVRG.....AGVCRCKLTSSGKCPTGFPK 45

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
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24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	259	100.0	45	2	AAP10385	Antitumour agent f
2	259	100.0	45	6	AAP50480	Cytostatic polypep
3	259	100.0	45	15	AAR60045	Alpha-hordothionin
4	259	100.0	45	19	AAW41689	Wild type barley a
5	247	95.4	45	15	AAR60047	Alpha-hordothionin
6	244	94.2	45	15	AAR60046	Alpha-hordothionin
7	243	93.8	45	13	AAR26858	Antifungal peptide
8	235	90.7	45	15	AAR60051	Alpha-hordothionin
9	231	89.2	45	13	AAR26859	Antifungal peptide
10	231	89.2	45	15	AAR60052	Alpha-hordothionin
11	231	89.2	45	18	AAW10163	Alpha-hordothionin
12	231	89.2	45	19	AAW58555	High lysine deriva
13	231	89.2	45	19	AAW41690	Methionine substit
14	225	86.9	45	13	AAR26860	Antifungal peptide
15	225	86.9	45	15	AAR60048	Alpha-hordothionin
16	224	86.5	45	2	AAP10126	Sequence of antitu
17	224	86.5	45	2	AAP10420	Anticancer compsn.
18	224	86.5	45	12	AAR12496	Alpha1-purothionin
19	224	86.5	45	24	AAE34437	Wheat thionin pept
20	214	82.6	45	2	AAP10125	Sequence of antitu
21	214	82.6	45	12	AAR12497	Alpha2-purothionin
22	214	82.6	45	12	AAR12498	Beta-purothionine.
23	214	82.6	45	13	AAR26861	Antifungal peptide
24	213	82.2	45	2	AAP10419	Anticancer compsn.
25	209	80.7	45	15	AAR60049	Alpha-hordothionin
26	202	78.0	45	15	AAR60050	Alpha-hordothionin
27	200	77.2	45	2	AAP10124	Generic sequence o
28	200	77.2	45	18	AAW10166	Alpha-hordothionin
29	184	71.0	45	18	AAW15300	Alpha-hordothionin
30	182	70.3	45	18	AAW10164	Alpha-hordothionin
31	182	70.3	45	19	AAW41691	Methionine substit
32	170	65.6	45	18	AAW10165	Alpha-hordothionin
33	169	65.3	45	15	AAR60053	Alpha-hordothionin
34	169	65.3	45	18	AAW10162	Alpha-hordothionin
35	166.5	64.3	46	19	AAW66467	Cationic peptide t
36	166.5	64.3	46	21	AAY91766	Cationic peptide T
37	166.5	64.3	46	24	ABU59644	Cationic cancer -t
38	154.5	59.7	46	17	AAW09637	Oat derived thioni
39	154.5	59.7	137	17	AAW09638	Oat-derived thioni
40	146	56.4	47	23	AAU97423	Pyrularia thionin,
41	146	56.4	48	18	AAW09616	Pyrularia pubera t
42	115.5	44.6	46	23	AAU97424	Viscotoxin A3 thio
43	115.5	44.6	46	23	AAU97426	Viscotoxin A2 thio
44	114.5	44.2	46	23	AAU97425	Viscotoxin B thion
45	114.5	44.2	46	23	AAU97427	Phoradendron thion

ALIGNMENTS

RESULT 1
AAP10385
ID AAP10385 standard; protein; 45 AA.
XX
AC AAP10385;
XX
DT 25-MAR-2003 (updated)
DT 10-MAR-2003 (updated)
DT 17-DEC-1992 (first entry)
XX
DE Antitumour agent from barley or wheat.
XX
KW antitumour; cancer; Ehrlich's ascites carcinoma; sarcoma 180A;
KW lymphocytic leukaemia L1210; triticum monococcum;
KW hordeum agriocrithon; hordeum spontaneum.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 3..39
FT Disulfide-bond 4..31
FT Disulfide-bond 12..29
FT Disulfide-bond 16..25
XX
PN JP56049342-A.
XX
PD 02-MAY-1981.
XX
PF 29-SEP-1979; 79JP-0126024.
XX
PR 29-SEP-1979; 79JP-0126024.
XX

```
PA   (SUNC ) SUN CHEM CORP.
XX
DR   WPI; 1981-45128D/25  (45128D).
XX
PT   Polypeptide antitumour agent - isolated from barley or wheat
XX
PS   Claim 1; Page 1; 7pp; Japanese.
XX
CC   This sequence represents an antitumour agent, abundant in wheat and
CC   barley. It is effective in the inhibition of the growth of
CC   transformed cells (released from contact inhibition) in a tissue
CC   culture test using mouse cell PV4. It is also effective against
CC   Ehrlichs ascites carcinoma , Sarcoma 180A, and lymphocyte leukaemia
CC   L1210 in mice.
CC   (Updated on 10-MAR-2003 to add missing OS field.)
CC   (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ   Sequence   45 AA;

  Query Match             100.0%;  Score 259;  DB 2;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-20;
  Matches   45;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              |||||||||||||||||||||||||||||||||||||||||||||
Db          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45


RESULT 2
AAP50480
ID   AAP50480 standard; peptide; 45 AA.
XX
AC   AAP50480;
XX
DT   28-NOV-1991  (first entry)
XX
DE   Cytostatic polypeptide SPH.
XX
KW   Cytostatic.
XX
OS   Triticum monococcum, Hordeum agriocrithon.
XX
FH   Key             Location/Qualifiers
FT   Disulfide-bond  3..39
FT   Disulfide-bond  4..31
FT   Disulfide-bond  12..29
FT   Disulfide-bond  16..25
XX
PN   US4497799-A.
XX
PD   05-FEB-1985.
XX
PF   09-NOV-1981;   81US-0319755.
XX
PR   09-NOV-1981;   81US-0319755.
XX
PA   (SUNR ) SUNTORY LTD.
XX
PI   Yoshizumi H,  Toyoshima K,  Hakura A,  Nakanishi T;
XX
DR   WPI; 1985-049834/08.
XX
PT   Inhibiting growth of transplanted tumours in mice - by admin of
PT   polypeptide SPH obtd. from cereals by solvent extn.,
PT   chromatography etc.
XX
PS   Claim 1; Page 6; 6pp; English.
XX
CC   The sequence encodes cycostatic polypeptide SPH, which is active
CC   against sarcomas, Ehrlich ascites carcinome and leukemia.
XX
SQ   Sequence   45 AA;

  Query Match             100.0%;  Score 259;  DB 6;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-20;
  Matches   45;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              |||||||||||||||||||||||||||||||||||||||||||||
Db          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45


RESULT 3
AAR60045
ID   AAR60045 standard; protein; 45 AA.
XX
AC   AAR60045;
XX
DT   25-MAR-2003  (updated)
DT   16-FEB-1995  (first entry)
XX
DE   Alpha-hordothionin.
XX
KW   Alpha-hordothionin; lysine; antifungal; antimicrobial;
KW   fungus resistance; disease resistance; crop improvement;
KW   crop protection; transgenic plant.
XX
OS   Hordeum vulgare.
XX
PN   WO9416078-A1.
XX
PD   21-JUL-1994.
XX
PF   12-JAN-1994;   94WO-US00382.
XX
PR   13-JAN-1993;   93US-0003885.
XX
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Beach LR,  Rao AG,  Rao A;
XX
DR   WPI; 1994-249225/30.
XX
PT   Derivatives of alpha hordothionin - have high lysine content, and
PT   retain antifungal activity of parent compound
XX
PS   Disclosure; Page 16; 27pp; English.
XX
CC   Lysine-rich alpha-hordothionin has powerful antifungal properties.
CC   Derivatives of alpha-hordothionin (given in AAR60046-53), made by
CC   position-specific substitution with lysine residues, provide
CC   improved resistance to fungal pathogens when expressed in
CC   transgenic dicot or monocot plants.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence   45 AA;

  Query Match             100.0%;  Score 259;  DB 15;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-20;
  Matches   45;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              |||||||||||||||||||||||||||||||||||||||||||||
Db          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45


RESULT 4
AAW41689
ID   AAW41689 standard; protein; 45 AA.
XX
AC   AAW41689;
XX
DT   01-MAY-1998  (first entry)
XX
DE   Wild type barley alpha-hordothionin.
XX
```

KW Phytopathogenic microorganism; alpha-hordothionin; barley;
KW essential amino acid methionine; feed formulation; anti-pathogenic.
XX
OS Hordeum vulgare.
XX
PN US5703049-A.
XX
PD 30-DEC-1997.
XX
PF 29-FEB-1996; 96US-0608786.
XX
PR 29-FEB-1996; 96US-0608786.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Rao AG;
XX
DR WPI; 1998-076460/07.
XX
PT Killing and inhibiting phytopathogenic microorganisms - by
PT expressing methionine rich alpha-hordothionin, useful in, e.g.
PT improving plant feed formulations
XX
PS Claim 1; Columns 7-8; 6pp; English.
XX
CC Killing and inhibiting phytopathogenic microorganisms, which are
CC susceptible to alpha-hordothionin, comprises introducing into the
CC environment of the microorganisms the protein AAW41691, in which at
CC least 1 of the amino acid residues at positions 1, 5, 8, 11, 15,
CC 17, 18, 19, 22, 23, 24, 30, 32, 33, 38 and 41 is replaced by
CC methionine, and the remainder of the residues at those positions
CC are the residues at the corresponding positions in the protein
CC AAW41689, e.g. AAW41690. The method may be used to improve feed
CC formulations, where derivatives of alpha-hordothionin are added to
CC provide higher percentages of the essential amino acid methionine
CC in plants, while retaining the anti-pathogenic functionality of
CC hordothionins. Alpha-Hordothionins may be expressed to
CC simultaneously enhance both resistance to plant pathogens, and
CC methionine content in plants.
XX
SQ Sequence 45 AA;

Query Match 100.0%; Score 259; DB 19; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.4e-20;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
||||||||||||||||||||||||||||||||||||||||||||
Db 1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45

RESULT 5
AAR60047
ID AAR60047 standard; protein; 45 AA.
XX
AC AAR60047;
XX
DT 25-MAR-2003 (updated)
DT 16-FEB-1995 (first entry)
XX
DE Alpha-hordothionin derivative.
XX
KW Alpha-hordothionin; lysine; antifungal; antimicrobial;
KW fungus resistance; disease resistance; crop improvement;
KW crop protection; transgenic plant.
XX
OS Hordeum vulgare.
XX
PN WO9416078-A1.
XX
PD 21-JUL-1994.
XX
PF 12-JAN-1994; 94WO-US00382.
XX
PR 13-JAN-1993; 93US-0003885.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Beach LR, Rao AG, Rao A;
XX
DR WPI; 1994-249225/30.
XX
PT Derivatives of alpha hordothionin - have high lysine content, and
PT retain antifungal activity of parent compound
XX
PS Disclosure; Page 17; 27pp; English.
XX
CC Lysine-rich alpha-hordothionin has powerful antifungal properties.
CC Derivatives of alpha-hordothionin (given in AAR60046-53), made by
CC position-specific substitution with lysine residues, provide
CC improved resistance to fungal pathogens when expressed in
CC transgenic dicot or monocot plants. Substitution of amino
CC acids 5, 17 and 19 of the wild-type sequence (AAR60045) with Lys
CC gave the protein given in AAR60047.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 45 AA;

Query Match 95.4%; Score 247; DB 15; Length 45;
Best Local Similarity 91.1%; Pred. No. 4.4e-19;
Matches 41; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
|||| :|||||||||||:|:||||||||||:|||||||||||||||
Db 1 KSCCKSTLGRNCYNLCKVKGAQKLCAGVCKCKLTSSGKCPTGFPK 45

RESULT 6
AAR60046
ID AAR60046 standard; protein; 45 AA.
XX
AC AAR60046;
XX
DT 25-MAR-2003 (updated)
DT 16-FEB-1995 (first entry)
XX
DE Alpha-hordothionin derivative.
XX
KW Alpha-hordothionin; lysine; antifungal; antimicrobial;
KW fungus resistance; disease resistance; crop improvement;
KW crop protection; transgenic plant.
XX
OS Hordeum vulgare.
XX
PN WO9416078-A1.
XX
PD 21-JUL-1994.
XX
PF 12-JAN-1994; 94WO-US00382.
XX
PR 13-JAN-1993; 93US-0003885.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Beach LR, Rao AG, Rao A;
XX
DR WPI; 1994-249225/30.
XX
PT Derivatives of alpha hordothionin - have high lysine content, and
PT retain antifungal activity of parent compound
XX
PS Disclosure; Page 16-17; 27pp; English.
XX
CC Lysine-rich alpha-hordothionin has powerful antifungal properties.
CC Derivatives of alpha-hordothionin (given in AAR60046-53), made by
CC position-specific substitution with lysine residues, provide

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CC   improved resistance to fungal pathogens when expressed in
CC   transgenic dicot or monocot plants.  Substitution of amino
CC   acids 5, 10, 19 and 30 of the wild-type sequence (AAR60045) with Lys
CC   gave the protein given in AAR60046.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence   45 AA;

  Query Match             94.2%;  Score 244;  DB 15;  Length 45;
  Best Local Similarity   88.9%;  Pred. No. 9.1e-19;
  Matches   40;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              ||||:||||:||||||:|:||||||||||:|||||||||||||||
Db          1 KSCCKSTLGKNCYNLCKVKGAQKLCAGVCKCKLTSSGKCPTGFPK 45


RESULT 7
AAR26858
ID   AAR26858 standard; peptide; 45 AA.
XX
AC   AAR26858;
XX
DT   25-MAR-2003  (updated)
DT   11-FEB-1993  (first entry)
XX
DE   Antifungal peptide #9.
XX
KW   Antimicrobial peptide; non-phytotoxic vehicle; fungal pathogen;
KW   expression cassette.
XX
OS   Synthetic.
XX
PN   EP502718-A1.
XX
PD   09-SEP-1992.
XX
PF   04-MAR-1992;   92EP-0301868.
XX
PR   04-MAR-1991;   91US-0664270.
XX
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Duvick J,  Rood T;
XX
DR   WPI; 1992-302013/37.
XX
PT   Treatment of bacterial and fungal infections - using natural and
PT   synthetic proteins e.g. adrenocorticotropic hormone, magainin,
PT   poly-L-arginine, mastoparan, kassinin etc.
XX
PS   Disclosure; Table 4; 21pp; English.
XX
CC   The peptides given in AAR26850-61 have been shown to have potent
CC   antimicrobial activity against many common pathogens.  They are
CC   particularly effective against fungal pathogens.  These peptides
CC   can be effectively applied to plants afflicted by susceptible
CC   microorganisms or they can be incorporated systematically into the
CC   tissues of a treated plant so that the infecting microbes are exposed
CC   to the pathogens in the course of the infection.  This may be done by
CC   incorporating the peptides into a non-phytotoxic vehicle adapted for
CC   systematic administration to the susceptible plants or by isolating
CC   the genes encoding them, inserting the genes into an appropriate
CC   expression cassette and using this to insert the gene of interest into
CC   the genome of the plant.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence   45 AA;

  Query Match             93.8%;  Score 243;  DB 13;  Length 45;
  Best Local Similarity   95.6%;  Pred. No. 1.2e-18;
  Matches   43;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              |||||||||||||||||||||||||||||||||||||||||| |||| ||
Db          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGLCPTGKPK 45


RESULT 8
AAR60051
ID   AAR60051 standard; protein; 45 AA.
XX
AC   AAR60051;
XX
DT   25-MAR-2003  (updated)
DT   16-FEB-1995  (first entry)
XX
DE   Alpha-hordothionin derivative.
XX
KW   Alpha-hordothionin; lysine; antifungal; antimicrobial;
KW   fungus resistance; disease resistance; crop improvement;
KW   crop protection; transgenic plant.
XX
OS   Hordeum vulgare.
XX
PN   WO9416078-A1.
XX
PD   21-JUL-1994.
XX
PF   12-JAN-1994;   94WO-US00382.
XX
PR   13-JAN-1993;   93US-0003885.
XX
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Beach LR,  Rao AG,  Rao A;
XX
DR   WPI; 1994-249225/30.
XX
PT   Derivatives of alpha hordothionin - have high lysine content, and
PT   retain antifungal activity of parent compound
XX
PS   Disclosure; Page 19; 7pp; English.
XX
CC   Lysine-rich alpha-hordothionin has powerful antifungal properties.
CC   Derivatives of alpha-hordothionin (given in AAR60046-53), made by
CC   position-specific substitution with lysine residues, provide
CC   improved resistance to fungal pathogens when expressed in
CC   transgenic dicot or monocot plants.  Substitution of amino
CC   acids 5, 11, 17, 19, 30 and 41 of the wild-type sequence
CC   (AAR60045) with Lys gave the protein given in AAR60051.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence   45 AA;

  Query Match             90.7%;  Score 235;  DB 15;  Length 45;
  Best Local Similarity   86.7%;  Pred. No. 8.1e-18;
  Matches   39;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              ||||:||||| |||||:|:||||||||||:|||||||||| ||||
Db          1 KSCCKSTLGRKCYNLCKVKGAQKLCAGVCKCKLTSSGKCPKGFPK 45


RESULT 9
AAR26859
ID   AAR26859 standard; peptide; 45 AA.
XX
AC   AAR26859;
XX
DT   25-MAR-2003  (updated)
DT   11-FEB-1993  (first entry)
XX
DE   Antifungal peptide #10.
XX
KW   Antimicrobial peptide; non-phytotoxic vehicle; fungal pathogen;
```

KW expression cassette.
XX
OS Synthetic.
XX
PN EP502718-A1.
XX
PD 09-SEP-1992.
XX
PF 04-MAR-1992; 92EP-0301868.
XX
PR 04-MAR-1991; 91US-0664270.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Duvick J, Rood T;
XX
DR WPI; 1992-302013/37.
XX
PT Treatment of bacterial and fungal infections - using natural and
PT synthetic proteins e.g. adrenocorticotropic hormone, magainin,
PT poly-L-arginine, mastoparan, kassinin etc.
XX
PS Disclosure; Table 4; 21pp; English.
XX
CC The peptides given in AAR26850-61 have been shown to have potent
CC antimicrobial activity against many common pathogens. They are
CC particularly effective against fungal pathogens. These peptides
CC can be effectively applied to plants afflicted by susceptible
CC microorganisms or they can be incorporated systematically into the
CC tissues of a treated plant so that the infecting microbes are exposed
CC to the pathogens in the course of the infection. This may be done by
CC incorporating the peptides into a non-phytotoxic vehicle adapted for
CC systematic administration to the susceptible plants or by isolating
CC the genes encoding them, inserting the genes into an appropriate
CC expression cassette and using this to insert the gene of interest into
CC the genome of the plant.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 45 AA;

Query Match 89.2%; Score 231; DB 13; Length 45;
Best Local Similarity 88.9%; Pred. No. 2.1e-17;
Matches 40; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
||||||||||||||||||||||||| ||||||| |||:||||
Db 1 KSCCRSTLGRNCYNLCRVRGAQKLCANACRCKLTSGLKCPSGFPK 45

RESULT 10
AAR60052
ID AAR60052 standard; protein; 45 AA.
XX
AC AAR60052;
XX
DT 25-MAR-2003 (updated)
DT 16-FEB-1995 (first entry)
XX
DE Alpha-hordothionin derivative.
XX
KW Alpha-hordothionin; lysine; antifungal; antimicrobial;
KW fungus resistance; disease resistance; crop improvement;
KW crop protection; transgenic plant.
XX
OS Hordeum vulgare.
XX
PN WO9416078-A1.
XX
PD 21-JUL-1994.
XX
PF 12-JAN-1994; 94WO-US00382.
XX
PR 13-JAN-1993; 93US-0003885.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Beach LR, Rao AG, Rao A;
XX
DR WPI; 1994-249225/30.
XX
PT Derivatives of alpha hordothionin - have high lysine content, and
PT retain antifungal activity of parent compound
XX
PS Disclosure; Page 19-20; 7pp; English.
XX
CC Lysine-rich alpha-hordothionin has powerful antifungal properties.
CC Derivatives of alpha-hordothionin (given in AAR60046-53), made by
CC position-specific substitution with lysine residues, provide
CC improved resistance to fungal pathogens when expressed in
CC transgenic dicot or monocot plants. Substitution of amino
CC acids 5, 11, 17, 19, 22, 30 and 41 of the wild-type sequence
CC (AAR60045) with Lys gave the protein given in AAR60052.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 45 AA;

Query Match 89.2%; Score 231; DB 15; Length 45;
Best Local Similarity 84.4%; Pred. No. 2.1e-17;
Matches 38; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
||||:||||| ||||:|:||:|||||||:|||||||||| ||||
Db 1 KSCCKSTLGRKCYNLCKVKGAKKLCAGVCKCKLTSSGKCPKGFPK 45

RESULT 11
AAW10163
ID AAW10163 standard; protein; 45 AA.
XX
AC AAW10163;
XX
DT 15-JUL-1997 (first entry)
XX
DE Alpha-hordothionin high methionine amino acid sequence.
XX
KW Animal feed; food; barley.
XX
OS Hordeum vulgare.
OS Synthetic.
XX
PN WO9638563-A1.
XX
PD 05-DEC-1996.
XX
PF 31-MAY-1996; 96WO-US08220.
XX
PR 02-JUN-1995; 95US-0460440.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Rao GA;
XX
DR WPI; 1997-034376/03.
XX
PT New modified alpha-hordothionin having methionine amino acid
PT substns. - to increase the methionine content of e.g. animal feed
XX
PS Claim 5; Page 11; 21pp; English.
XX
CC The present sequence is an example of a methionine rich modified alpha-
CC hordothionin amino acid sequence. The protein contains a methionine
CC residue at positions 8, 11, 15, 18, 22, 33, and 41, replacing the surface
CC hydrophobic residues (leucine at positions 8, 15 and 33, and valine at
CC position 18), and the surface polar residues (asparagine at position 11,
CC glutamine at position 22 and threonine at position 41). The molecule is
CC synthesised by solid phase peptide synthesis and folds into a stable

```
CC   structure. The modified protein has a sulphur amino acid content of 33%.
CC   The protein produced can be used in foods or feeds to provide higher
CC   levels of essential amino acid methionine.
XX
SQ   Sequence   45 AA;

  Query Match             89.2%;  Score 231;  DB 18;  Length 45;
  Best Local Similarity   84.4%;  Pred. No. 2.1e-17;
  Matches   38;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              |||||||:|| |||:||:||| ||||||||||:||||||| ||||
Db          1 KSCCRSTMGRMCYNMCRMRGAMKLCAGVCRCKMTSSGKCPMGFPK 45


RESULT 12
AAW58555
ID   AAW58555 standard; protein; 45 AA.
XX
AC   AAW58555;
XX
DT   03-SEP-1998  (first entry)
XX
DE   High lysine derivative of alpha-hordothionine.
XX
KW   Alpha-hordothionine; lysine; maize; photosynthetic organ; barley;
KW   transgenic plant; seed; animal feed; nutrition; engineered.
XX
OS   Hordeum vulgare.
XX
PN   WO9813506-A1.
XX
PD   02-APR-1998.
XX
PF   17-SEP-1997;   97WO-US16111.
XX
PR   25-SEP-1996;   96US-0719500.
XX
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Staswick PE,  Tarczynski MC;
XX
DR   WPI; 1998-286414/25.
XX
PT   Transgenic plants engineered to express essential amino acids in
PT   seed - useful in the production of animal feed compositions
XX
PS   Example 3; Page 32; 41pp; English.
XX
CC   The present sequence represents a high lysine derivative of
CC   alpha-hordothionine, used in an example of the present invention for its
CC   expression in maize photosynthetic organs. The present invention
CC   describes plants, which express an altered composition or quantity (i.e.
CC   increased yield) of a vegetative storage protein, which are genetically
CC   modified to have a higher yield than the wild-type by: (a) expressing a
CC   transgene encoding a target amino acid sequence (T) in an organ or
CC   tissue of the plant other than the seed; and (b) accumulating (T) in the
CC   organ or tissue. The transgenic plants are engineered to express an
CC   increased amount of a protein containing an increased amount of an
CC   essential amino acid in the seed. The seed can then be used as a fodder
CC   additive. The method is especially useful for the production of essential
CC   amino acids: methionine, cysteine, threonine and lysine; which are
CC   needed for animal nutrition but are often limited in crops.
XX
SQ   Sequence   45 AA;

  Query Match             89.2%;  Score 231;  DB 19;  Length 45;
  Best Local Similarity   84.4%;  Pred. No. 2.1e-17;
  Matches   38;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              ||||:||||| |||||:|:||:|||||||:|||||||||| ||||
Db          1 KSCCKSTLGRKCYNLCKVKGAKKLCAGVCKCKLTSSGKCPKGFPK 45


RESULT 13
AAW41690
ID   AAW41690 standard; protein; 45 AA.
XX
AC   AAW41690;
XX
DT   01-MAY-1998  (first entry)
XX
DE   Methionine substituted barley alpha-hordothionin.
XX
KW   Phytopathogenic microorganism; alpha-hordothionin; barley;
KW   essential amino acid methionine; feed formulation; anti-pathogenic.
XX
OS   Hordeum vulgare.
OS   Synthetic.
XX
PN   US5703049-A.
XX
PD   30-DEC-1997.
XX
PF   29-FEB-1996;   96US-0608786.
XX
PR   29-FEB-1996;   96US-0608786.
XX
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Rao AG;
XX
DR   WPI; 1998-076460/07.
XX
PT   Killing and inhibiting phytopathogenic microorganisms - by
PT   expressing methionine rich alpha-hordothionin, useful in, e.g.
PT   improving plant feed formulations
XX
PS   Claim 1; Columns 9-10; 6pp; English.
XX
CC   Killing and inhibiting phytopathogenic microorganisms, which are
CC   susceptible to alpha-hordothionin, comprises introducing into the
CC   environment of the microorganisms the protein AAW41691, in which at
CC   least 1 of the amino acid residues at positions 1, 5, 8, 11, 15,
CC   17, 18, 19, 22, 23, 24, 30, 32, 33, 38 and 41 is replaced by
CC   methionine, and the remainder of the residues at those positions
CC   are the residues at the corresponding positions in the protein
CC   AAW41689, e.g. AAW41690. The method may be used to improve feed
CC   formulations, where derivatives of alpha-hordothionin are added to
CC   provide higher percentages of the essential amino acid methionine
CC   in plants, while retaining the anti-pathogenic functionality of
CC   hordothionins. Alpha-Hordothionins may be expressed to
CC   simultaneously enhance both resistance to plant pathogens, and
CC   methionine content in plants.
XX
SQ   Sequence   45 AA;

  Query Match             89.2%;  Score 231;  DB 19;  Length 45;
  Best Local Similarity   84.4%;  Pred. No. 2.1e-17;
  Matches   38;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              |||||||:|| |||:||:||| ||||||||||:||||||| ||||
Db          1 KSCCRSTMGRMCYNMCRMRGAMKLCAGVCRCKMTSSGKCPMGFPK 45


RESULT 14
AAR26860
ID   AAR26860 standard; peptide; 45 AA.
XX
AC   AAR26860;
XX
DT   25-MAR-2003  (updated)
DT   11-FEB-1993  (first entry)
XX
```

DE Antifungal peptide #11.
XX
KW Antimicrobial peptide; non-phytotoxic vehicle; fungal pathogen;
KW expression cassette.
XX
OS Synthetic.
XX
PN EP502718-A1.
XX
PD 09-SEP-1992.
XX
PF 04-MAR-1992; 92EP-0301868.
XX
PR 04-MAR-1991; 91US-0664270.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Duvick J, Rood T;
XX
DR WPI; 1992-302013/37.
XX
PT Treatment of bacterial and fungal infections - using natural and
PT synthetic proteins e.g. adrenocorticotropic hormone, magainin,
PT poly-L-arginine, mastoparan, kassinin etc.
XX
PS Disclosure; Table 4; 21pp; English.
XX
CC The peptides given in AAR26850-61 have been shown to have potent
CC antimicrobial activity against many common pathogens. They are
CC particularly effective against fungal pathogens. These peptides
CC can be effectively applied to plants afflicted by susceptible
CC microorganisms or they can be incorporated systematically into the
CC tissues of a treated plant so that the infecting microbes are exposed
CC to the pathogens in the course of the infection. This may be done by
CC incorporating the peptides into a non-phytotoxic vehicle adapted for
CC systematic administration to the susceptible plants or by isolating
CC the genes encoding them, inserting the genes into an appropriate
CC expression cassette and using this to insert the gene of interest into
CC the genome of the plant.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 45 AA;

Query Match 86.9%; Score 225; DB 13; Length 45;
Best Local Similarity 86.7%; Pred. No. 9e-17;
Matches 39; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              |||||||||||||||||||||||||||  ||||||| |||: |||
Db          1 KSCCRSTLGRNCYNLCRVRGAQKLCANACRCKLTSGLKCPSSFPK 45
```

RESULT 15
AAR60048
ID AAR60048 standard; protein; 45 AA.
XX
AC AAR60048;
XX
DT 25-MAR-2003 (updated)
DT 16-FEB-1995 (first entry)
XX
DE Alpha-hordothionin derivative.
XX
KW Alpha-hordothionin; lysine; antifungal; antimicrobial;
KW fungus resistance; disease resistance; crop improvement;
KW crop protection; transgenic plant.
XX
OS Hordeum vulgare.
XX
PN WO9416078-A1.
XX
PD 21-JUL-1994.
XX
PF 12-JAN-1994; 94WO-US00382.
XX
PR 13-JAN-1993; 93US-0003885.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Beach LR, Rao AG, Rao A;
XX
DR WPI; 1994-249225/30.
XX
PT Derivatives of alpha hordothionin - have high lysine content, and
PT retain antifungal activity of parent compound
XX
PS Disclosure; Page 17-18; 7pp; English.
XX
CC Lysine-rich alpha-hordothionin has powerful antifungal properties.
CC Derivatives of alpha-hordothionin (given in AAR60046-53), made by
CC position-specific substitution with lysine residues, provide
CC improved resistance to fungal pathogens when expressed in
CC transgenic dicot or monocot plants. Substitution of amino
CC acids 5, 12, 17, 19 and 30 of the wild-type sequence (AAR60045)
CC with Lys, and of Cys-29 with Thr, gave the protein given in
CC AAR60048.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 45 AA;

Query Match 86.9%; Score 225; DB 15; Length 45;
Best Local Similarity 86.7%; Pred. No. 9e-17;
Matches 39; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 KSCCRSTLGRNCYNLCRVRGAQKLCAGVCRCKLTSSGKCPTGFPK 45
              ||||:|||||| ||||:|:|||||||| :|||||||||||||||
Db          1 KSCCKSTLGRNKYNLCKVKGAQKLCAGVTKCKLTSSGKCPTGFPK 45
```

Search completed: January 21, 2004, 09:47:14
Job time : 42 secs